PCT/GB 2003 / 0 0 4 6 3 6

INVESTOR IN PEOPLE

The Patent Office
Concept House
Cardiff Road
Newport
South Wales
NP10 8QQ

PRIORITY DOCUMENT
SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH
RULE 17.1(a) OR (b)

REC'D 11 DEC 2003
WIPO PCT

I, the undersigned, being an officer duly authorised in accordance with Section 74(1) and (4) of the Deregulation & Contracting Out Act 1994, to sign and issue certificates on behalf of the Comptroller-General, hereby certify that annexed hereto is a true copy of the documents as originally filed in connection with the patent application identified therein.

In accordance with the Patents (Companies Re-registration) Rules 1982, if a company named in this certificate and any accompanying documents has re-registered under the Companies Act 1980 with the same name as that with which it was registered immediately before re-registration save for the substitution as, or inclusion as, the last part of the name of the words "public limited company" or their equivalents in Welsh, references to the name of the company in this certificate and any accompanying documents shall be treated as references to the name with which it is so re-registered.

In accordance with the rules, the words "public limited company" may be replaced by p.l.c., plc, P.L.C. or PLC.

Re-registration under the Companies Act does not constitute a new legal entity but merely subjects the company to certain additional company law rules.

Signed

Dated 11 November 2003

Patents Form 1/77

Patents Act 1977
(Rule 16)

Request for grant of a patent

(See the notes on the back of this form. You can also get an explanatory leaflet from the Patent Office to help you fill in this form)

The Patent Office

Cardiff Road
Newport
South Wales
NP10 8QQ

1. Your reference

CASE NO 43

2. Patent application number
(The Patent Office will fill in this part)

0316356.5

11 JUL 2003

3. Full name, address and postcode of the or of each applicant *(underline all surnames)*

AVIDEX LTD
57C MILTON PARK
ABINGDON
OXFORDSHIRE
OX14 4RX

Patents ADP number *(if you know it)* 8571242001

If the applicant is a corporate body, give the country/state of its incorporation ENGLAND

4. Title of the invention

SUBSTANCES

5. Name of your agent *(if you have one)*

"Address for service" in the United Kingdom to which all correspondence should be sent *(including the postcode)*

MR ALAN WALLS
AVIDEX LTD
57C MILTON PARK
ABINGDON
OXFORDSHIRE
OX14 4RX

Patents ADP number *(if you know it)* 8571242001

6. If you are declaring priority from one or more earlier patent applications, give the country and the date of filing of the or of each of these earlier applications and *(if you know it)* the or each application number

Country	Priority application number *(if you know it)*	Date of filing *(day / month / year)*

7. If this application is divided or otherwise derived from an earlier UK application, give the number and the filing date of the earlier application

Number of earlier application	Date of filing *(day / month / year)*

8. Is a statement of inventorship and of right to grant of a patent required in support of this request? *(Answer 'Yes' if:*

a) any applicant named in part 3 is not an inventor, or
b) there is an inventor who is not named as an applicant, or
c) any named applicant is a corporate body.
See note (d))

YES

Patents Form 1/77

9. Enter the number of sheets for any of the following items you are filing with this form. Do not count copies of the same document

Continuation sheets of this form	
Description	79 ✓
Claim(s)	12 ✓
Abstract	0
Drawing(s)	3+3+4 JML

10. If you are also filing any of the following, state how many against each item.

Priority documents	
Translations of priority documents	
Statement of inventorship and right to grant of a patent *(Patents Form 7/77)*	
Request for preliminary examination and search *(Patents Form 9/77)*	
Request for substantive examination *(Patents Form 10/77)*	
Any other documents *(please specify)*	

11. I/We request the grant of a patent on the basis of this application.

Signature Alan N Walls Date 11th July 2003

12. Name and daytime telephone number of person to contact in the United Kingdom Mr MARTIN GREEN (01235) 435612

Warning

After an application for a patent has been filed, the Comptroller of the Patent Office will consider whether publication or communication of the invention should be prohibited or restricted under Section 22 of the Patents Act 1977. You will be informed if it is necessary to prohibit or restrict your invention in this way. Furthermore, if you live in the United Kingdom, Section 23 of the Patents Act 1977 stops you from applying for a patent abroad without first getting written permission from the Patent Office unless an application has been filed at least 6 weeks beforehand in the United Kingdom for a patent for the same invention and either no direction prohibiting publication or communication has been given, or any such direction has been revoked.

Notes

a) If you need help to fill in this form or you have any questions, please contact the Patent Office on 08459 500505.

b) Write your answers in capital letters using black ink or you may type them.

c) If there is not enough space for all the relevant details on any part of this form, please continue on a separate sheet of paper and write "see continuation sheet" in the relevant part(s). Any continuation sheet should be attached to this form.

d) If you have answered 'Yes' Patents Form 7/77 will need to be filed.

e) Once you have filled in the form you must remember to sign and date it.

f) For details of the fee and ways to pay please contact the Patent Office.

SUBSTANCES

The present invention relates to proteinaceous particles, for example phage or ribosome particles, displaying T cell receptors (TCRs).

Background to the Invention

Native TCRs

As is described in, for example, WO 99/60120 TCRs mediate the recognition of specific Major Histocompatibility Complex (MHC)-peptide complexes by T cells and, as such, are essential to the functioning of the cellular arm of the immune system.

Antibodies and TCRs are the only two types of molecules which recognise antigens in a specific manner, and thus the TCR is the only receptor for particular peptide antigens presented in MHC, the alien peptide often being the only sign of an abnormality within a cell. T cell recognition occurs when a T-cell and an antigen presenting cell (APC) are in direct physical contact, and is initiated by ligation of antigen-specific TCRs with pMHC complexes.

The native TCR is a heterodimeric cell surface protein of the immunoglobulin superfamily which is associated with invariant proteins of the CD3 complex involved in mediating signal transduction. TCRs exist in $\alpha\beta$ and $\gamma\delta$ forms, which are structurally similar but have quite distinct anatomical locations and probably functions. The MHC class I and class II ligands are also immunoglobulin superfamily proteins but are specialised for antigen presentation, with a highly polymorphic peptide binding site which enables them to present a diverse array of short peptide fragments at the APC cell surface.

Two further classes of proteins are known to be capable of functioning as TCR ligands. (1) CD1 antigens are MHC class I-related molecules whose genes are located on a different chromosome from the classical MHC class I and class II antigens. CD1 molecules are capable of presenting peptide and non-peptide (eg lipid, glycolipid)

moieties to T cells in a manner analogous to conventional class I and class II-MHC-pep complexes. See, for example (Barclay et al, (1997)The Leucocyte Antigen Factsbook 2nd Edition, Acadmeic Press) and (Bauer (1997) Eur J Immunol 27 (6) 1366-1373)) (2) Bacterial superantigens are soluble toxins which are capable of binding both class II MHC molecules and a subset of TCRs.(Fraser (1989) Nature 339 221-223) Many superantigens exhibit specificity for one or two Vbeta segments, whereas others exhibit more promiscuous binding. In any event, superantigens are capable of eliciting an enhanced immune response by virtue of their ability to stimulate subsets of T cells in a polyclonal fashion.

The extracellular portion of native heterodimeric αβ and γδ TCRs consist of two polypeptides each of which has a membrane-proximal constant domain, and a membrane-distal variable domain. Each of the constant and variable domains includes an intra-chain disulfide bond. The variable domains contain the highly polymorphic loops analogous to the complementarity determining regions (CDRs) of antibodies. CDR3 of αβ TCRs interact with the peptide presented by MHC, and CDRs 1 and 2 of αβ TCRs interact with the peptide and the MHC. The diversity of TCR sequences is generated via somatic rearrangement of linked variable (V), diversity (D), joining (J), and constant genes

Functional α and γ chain polypeptides are formed by rearranged V-J-C regions, whereas β and δ chains consist of V-D-J-C regions. The extracellular constant domain has a membrane proximal region and an immunoglobulin region. There are single α and δ chain constant domains, known as TRAC and TRDC respectively. The β chain constant domain is composed of one of two different β constant domains, known as TRBC1 and TRBC2 (IMGT nomenclature). There are four amino acid changes between these β constant domains, three of which are within the domains used to produce the single-chain TCRs displayed on phage particles of the present invention. These changes are all within exon 1 of TRBC1 and TRBC2:. N_4K_5->K_4N_5 and F_{37}->Y (IMGT numbering, differences TRBC1->TRBC2), the final amino acid change

between the two TCR β chain constant regions being in exon 3 of TRBC1 and TRBC2: V_1->E. The constant γ domain is composed of one of either TRGC1, TRGC2(2x) or TRGC2(3x). The two TRGC2 constant domains differ only in the number of copies of the amino acids encoded by exon 2 of this gene that are present.

The extent of each of the TCR extracellular domains is somewhat variable. However, a person skilled in the art can readily determine the position of the domain boundaries using a reference such as The T Cell Receptor Facts Book, Lefranc & Lefranc, Publ. Academic Press 2001.

Recombinant TCRs

The production of recombinant TCRs is beneficial as these provide soluble TCR analogues suitable for the following purposes:

- Studying the TCR / ligand interactions (e.g. pMHC for αβ TCRs)
- Screening for inhibitors of TCR-associated interactions
- Providing the basis for potential therapeutics

A number of constructs have been devised to date for the production of recombinant TCRs. These constructs fall into two broad classes, single-chain TCRs and dimeric TCRs, the literature relevant to these constructs is summarised below.

Single-chain TCRs (scTCRs) are artificial constructs consisting of a single amino acid strand, which like native heterodimeric TCRs bind to MHC-peptide complexes. Unfortunately, attempts to produce functional alpha/beta analogue scTCRs by simply linking the alpha and beta chains such that both are expressed in a single open reading frame have been unsuccessful, presumably because of the natural instability of the alpha-beta soluble domain pairing.

Accordingly, special techniques using various truncations of either or both of the alpha and beta chains have been necessary for the production of scTCRs. These formats appear to be applicable only to a very limited range of scTCR sequences. Soo Hoo *et*

al (1992) PNAS. **89** (10): 4759-63 report the expression of a mouse TCR in single chain format from the 2C T cell clone using a truncated beta and alpha chain linked with a 25 amino acid linker and bacterial periplasmic expression (see also Schodin *et al* (1996) Mol. Immunol. **33 (9)**: 819-29). This design also forms the basis of the m6 single-chain TCR reported by Holler *et al* (2000) PNAS. **97** (10): 5387-92 which is derived from the 2C scTCR and binds to the same H2-Ld-restricted alloepitope. Shusta *et al* (2000) Nature Biotechnology **18**: 754-759 and US 6,423,538 report using a murine single-chain 2C TCR constructs in yeast display experiments, which produced mutated TCRs with, enhanced thermal stability and solubility. This report also demonstrated the ability of these displayed 2C TCRs to selectively bind cells expressing their cognate pMHC. Khandekar *et al* (1997) J. Biol. Chem. **272** (51): 32190-7 report a similar design for the murine D10 TCR, although this scTCR was fused to MBP and expressed in bacterial cytoplasm (see also Hare *et al* (1999) Nat. Struct. Biol. **6** (6): 574-81). Hilyard *et al* (1994) PNAS. **91** (19): 9057-61 report a human scTCR specific for influenza matrix protein-HLA-A2, using a Vα-linker-Vβ design and expressed in bacterial periplasm.

Chung *et al* (1994) PNAS. **91** (26) 12654-8 report the production of a human scTCR using a Vα-linker-Vβ-Cβ design and expression on the surface of a mammalian cell line. This report does not include any reference to peptide-HLA specific binding of the scTCR. Plaksin *et al* (1997) J. Immunol. **158** (5): 2218-27 report a similar Vα-linker-Vβ-Cβ design for producing a murine scTCR specific for an HIV gp120-H-2D^{d} epitope. This scTCR is expressed as bacterial inclusion bodies and refolded *in vitro*.

A number of papers describe the production of TCR heterodimers which include the native disulphide bridge which connects the respective subunits (Garboczi, *et al.*, (1996), Nature **384**(6605): 134-41; Garboczi, *et al.*, (1996), J Immunol **157**(12): 5403-10; Chang *et al.*, (1994), PNAS USA **91**: 11408-11412; Davodeau *et al.*, (1993), *J. Biol. Chem.* **268**(21): 15455-15460; Golden *et al.*, (1997), J. Imm. Meth. **206**: 163-169; US Patent No. 6080840). However, although such TCRs can be recognised by

TCR-specific antibodies, none were shown to recognise its native ligand at anything other than relatively high concentrations and/or were not stable.

In WO 99/60120, a soluble TCR is described which is correctly folded so that it is capable of recognising its native ligand, is stable over a period of time, and can be produced in reasonable quantities. This TCR comprises a TCR α or γ chain extracellular domain dimerised to a TCR β or δ chain extracellular domain respectively, by means of a pair of C-terminal dimerisation peptides, such as leucine zippers. This strategy of producing TCRs is generally applicable to all TCRs.

Reiter *et al*, Immunity, 1995, **2**:281-287, details the construction of a soluble molecule comprising disulphide-stabilised TCR α and β variable domains, one of which is linked to a truncated form of Pseudomonas exotoxin (PE38). One of the stated reasons for producing this molecule was to overcome the inherent instability of single-chain TCRs. The position of the novel disulphide bond in the TCR variable domains was identified via homology with the variable domains of antibodies, into which these have previously been introduced (for example see Brinkmann, *et al.* (1993), Proc. Natl. Acad. Sci. USA **90:** 7538-7542, and Reiter, *et al.* (1994) Biochemistry **33:** 5451-5459). However, as there is no such homology between antibody and TCR constant domains, such a technique could not be employed to identify appropriate sites for new inter-chain disulphide bonds between TCR constant domains.

As mentioned above Shusta *et al* (2000) Nature Biotechnology **18**: 754-759 report using single-chain 2 C TCR constructs in yeast display experiments. The principle of displaying scTCRs on phage particles has previously been discussed. For example, WO 99/19129 details the production of scTCRs, and summarise a potential method for the production of phage particles displaying scTCRs of the Vα-Linker-Vβ Cβ format. However, this application contains no exemplification demonstrating the production of said phage particles displaying TCR. The application does however refer to a co-pending application:

"The construction of DNA vectors including a DNA segment encoding a sc-TCR molecules fused to a bacteriophage coat protein (gene II or gene VIII) have been described in said pending U.S. application No. 08/813,781."

Furthermore, this application relies on the ability of anti-TCR antibodies or super-antigen MHC complexes to recognise the soluble, non-phage displayed, scTCRs produced to verify their correct conformation. Therefore, true peptide-MHC binding specificity of the scTCRs, in any format, is not conclusively demonstrated.

Screening Use

A number of important cellular interactions and cell responses, including the TCR-mediated immune synapse, are controlled by contacts made between cell surface receptors and ligands presented on the surfaces of other cells. These types of specific molecular contacts are of crucial importance to the correct biochemical regulation in the human body and are therefore being studied intensely. In many cases, the objective of such studies is to devise a means of modulating cellular responses in order to prevent or combat disease.

Therefore, methods with which to identify compounds that bind with some degree of specificity to human receptor or ligand molecules are important as leads for the discovery and development of new disease therapeutics. In particular, compounds that interfere with certain receptor-ligand interactions have immediate potential as therapeutic agents or carriers.

Advances in combinatorial chemistry, enabling relatively easy and cost-efficient production of very large compound libraries have increased the scope for compound testing enormously. Now the limitations of screening programmes most often reside in the nature of the assays that can be employed, the production of suitable receptor and ligand molecules and how well these assays can be adapted to high throughput screening methods.

Display Methods

It is often desirable to present a given peptide or polypeptide on the surface of a proteinaceous particle. Such particles may serve as purification aids for the peptide or polypeptide (since the particles carrying the peptide or polypeptide may be separated from unwanted contaminants by sedimentation or other methods). They may also serve as particulate vaccines, the immune response to the surface displayed peptide or polypeptide being stimulated by the particulate presentation. Protein p24 of the yeast retrotransposon, and the hepatitis B surface coat protein are examples of proteins which self assemble into particles. Fusion of the peptide or polypeptide of interest to these particle-forming proteins is a recognised way of presenting the peptide or polypeptide on the surface of the resultant particles.

However, particle display methods have primarily been used to identify proteins with desirable properties such as enhanced expression yields, binding and/or stability characteristics. These methods involve creating a diverse pool or 'library' of proteins or polypeptides expressed on the surface of proteinaceous particles. These particles have two key features, firstly each particle presents a single variant protein or polypeptide, and secondly the genetic material encoding the expressed protein or polypeptide is associated with that of the particle. This library is then subjected to one or more rounds of selection. For example, this may consist of contacting a ligand with a particle-display library of mutated receptors and identifying which mutated receptors bind the ligand with the highest affinity. Once the selection process has been completed the receptor or receptors with the desired properties can be isolated, and their genetic material can be amplified in order to allow the receptors to be sequenced.

These display methods fall into two broad categories, *in-vitro* and *in-vivo* display.

All *in-vivo* display methods rely on a step in which the library, usually encoded in or with the genetic nucleic acid of a replicable particle such as a plasmid or phage replicon is transformed into cells to allow expression of the proteins or polypeptides. (Plückthun (2001) Adv Protein Chem **55** 367-403). There are a number of

replicon/host systems that have proved suitable for *in-vivo* display of protein or polypeptides. These include the following

Phage / bacterial cells

plasmid / CHO cells

Vectors based on the yeast 2μm plasmid / yeast cells

bacculovirus / insect cells

plasmid / bacterial cells

In-vivo display methods include cell-surface display methods in which a plasmid is introduced into the host cell encoding a fusion protein consisting of the protein or polypeptide of interest fused to a cell surface protein or polypeptide. The expression of this fusion protein leads to the protein or polypeptide of interest being displayed on the surface of the cell. The cells displaying these proteins or polypeptides of interest can then be subjected to a selection process such as FACS and the plasmids obtained from the selected cell or cells can be isolated and sequenced. Cell surface display systems have been devised for mammalian cells (Higuschi (1997) J Immunol. Methods **202** 193-204), yeast cells (Shusta (1999) J Mol Biol **292** 949-956) and bacterial cells (Sameulson (2002) J. Biotechnol **96** (2) 129-154).

Numerous reviews of the various in-vivo display techniques have been published. For example, (Hudson (2002) Expert Opin Biol Ther (2001) **1** (5) 845-55) and (Schmitz (2000) **21** (Supp A) S106-S112).

In-vitro display methods are based on the use of ribosomes to translate libraries of mRNA into a diverse array of protein or polypeptide variants. The linkage between the proteins or polypeptides formed and the mRNA encoding these molecules is maintained by one of two methods. Conventional ribosome display utilises mRNA sequences that encode a short (typically 40-100 amino acid) linker sequence and the protein or polypeptide to be displayed. The linker sequence allow the displayed

protein or polypeptide sufficient space to re-fold without being sterically hindered by the ribosme. The mRNA sequence lacks a 'stop' codon, this ensures that the expressed protein or polypeptide and the RNA remain attached to the ribosome particle. The related mRNA display method is based on the preparation of mRNA sequences encoding the protein or polypeptide of interest and DNA linkers carrying a puromycin moiety. As soon as the ribosome reaches the mRNA/DNA junction translation is stalled and the puromycin forms a covalent linkage to the ribosome. For a recent review of these two related *in-vitro* display methods see (Amstutz (2001) Curr Opin Biotechnol **12** 400-405).

Particularly preferred is the phage display technique which is based on the ability of bacteriophage particles to express a heterologous peptide or polypeptide fused to their surface proteins. (Smith (1985) Science **217** 1315-1317). The procedure is quite general, and well understood in the art for the display of polypeptide monomers. However, in the case of polypeptides that in their native form associate as dimers, only the phage display of antibodies appears to have been thoroughly investigated.

For monomeric polypeptide display there are two main procedures:
Firstly (Method A) by inserting into a vector (phagemid) DNA encoding the heterologous peptide or polypeptide fused to the DNA encoding a bacteriophage coat protein. The expression of phage particles displaying the heterologous peptide or polypeptide is then carried out by transfecting bacterial cells with the phagemid, and then infecting the transformed cells with a 'helper phage'. The helper phage acts as a source of the phage proteins not encoded by the phagemid required to produce a functional phage particle.

Secondly (Method B), by inserting DNA encoding the heterologous peptide or polypeptide into a complete phage genome fused to the DNA encoding a bacteriophage coat protein. The expression of phage particles displaying the heterologous peptide or polypeptide is then carried out by infecting bacterial cells with the phage genome. This method has the advantage of the first method of being a

'single-step' process. However, the size of the heterologous DNA sequence that can be successfully packaged into the resuting phage particles is reduced. M13, T7 and Lambda are examples of suitable phages for this method.

A variation on (Method B) the involves adding a DNA sequence encoding a nucleotide binding domain to the DNA in the phage genome encoding the heterologous peptide be displayed, and further adding the corresponding nucleotide binding site to the phage genome. This causes the heterologous peptide to become directly attached to the phage genome. This peptide/genome complex is then packaged into a phage particle which displays the heterologous peptide. This method is fully described in WO 99/11785.

The phage particles can then be recovered and used to study the binding characteristics of the heterologous peptide or polypeptide. Once isolated, phagemid or phage DNA can be recovered from the peptide- or polypeptide-displaying phage particle, and this DNA can be replicated via PCR. The PCR product can be used to sequence the heterologous peptide or polypeptide displayed by a given phage particle.

The phage display of single-chain antibodies and fragments thereof, has become a routine means of studying the binding characteristics of these polypeptides. There are numerous books available that review phage display techniques and the biology of the bacteriophage. (See, for example, Phage Display – A Laboratory Manual, Barbas *et al.*, (2001) Cold Spring Harbour Laboratory Press).

A third phage display method (Method C) relies on the fact that heterologous polypeptides having a cysteine residue at a desired location can be expressed in a soluble form by a phagemid or phage genome, and caused to associate with a modified phage surface protein also having a cysteine residue at a surface exposed position, via the formation of a disulphide linkage between the two cysteines. WO 01/ 05950 details the use of this alternative linkage method for the expression of single-chain antibody-derived peptides.

Brief Description of the Invention

Native TCR's are heterodimers which have lengthy transmembrane domains which are essential to maintain their stability as functional dimers. As discussed above, TCRs are useful for research and therapeutic purposes in their soluble forms so display of the insoluble native form has little utility. On the other hand, soluble stable forms of TCRs have proved difficult to design, and since most display methods appear to have been described only for monomeric peptides and polypeptides, display methods suitable for soluble dimeric TCRs have not been investigated. Furthermore, since the functionality of the displayed TCR depends on proper association of the variable regions of the TCR dimer, successful display of a functional dimeric TCR is not trivial.

WO 99/18129 contains the statement: "DNA constructs encoding the sc-TCR fusion proteins can be used to make a bacteriophage display library in accordance with methods described in pending U.S. application Serial No. 08/813.781 filed on March 7, 1997, the disclosure of which is incorporated herein by reference.", but no actual description of such display is included in this application. However, The inventors of this application published a paper (Weidanz (1998) J Immunol Methods 221 59-76) that demonstrates the display of two murine scTCRs on phage particles.

WO 01/62908 discloses methods for the phage display of scTCRs and scTCR/ Ig fusion proteins. However, the functionality (specific pMHC binding) of the constructs disclosed was not assessed.

Finally, a retrovirus-mediated method for the display of diverse TCR libraries on the surface of immature T cells has been demonstrated for a murine TCR. The library of mutated TCRs displayed of the surface of the immature T cells was screened by flow cytometry using pMHC tetramers, and this lead to the identification TCR variants that were either specific for the cognate pMHC, or a variant thereof. (Helmut *et al.*, (2000) PNAS **97** (26) 14578-14583)

This invention is based in part on the finding that single chain and dimeric TCRs can be expressed as surface fusions to proteinaceous particles, and makes available proteinaceous particles displaying alpha/beta-analogue and gamma/delta-analogue scTCR and dTCR constructs. The proteinaceous particles on which the TCRs are displayed include self-aggregating particle-forming proteins, phage, virus-derived and ribosome particles. Such proteinaceous particle-displayed TCRs are useful for purification and screening purposes, particularly as a diverse library of particle displayed TCRs for biopanning to identify TCRs with desirable characteristics such as strong affinity for the target MHC-peptide complex. In the latter connection, particle-displayed scTCRs may be useful for identification of the desired TCR, but that information may be better applied to the construction of analogous dimeric TCRs for ultimate use in therapy.

Detailed Description of the Invention

The present invention provides a proteinaceous particle displaying on its surface a T-cell receptor(TCR), characterised in that

(i) the proteinaceous particle is a ribosome and the TCR is a single chain TCR (scTCR) polypeptide, or

(ii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a human scTCR or a human dimeric T-cell receptor (dTCR) polypeptide pair, or

(iii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a non-human dTCR polypeptide pair, or

(iv) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a scTCR polypeptide comprising TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the

latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain, and a disulfide bond which has no equivalent in native T cell receptors links residues of the constant region sequences.

In a preferred embodiment, the invention provides a proteinaceous particle displaying on its surface a dimeric T-cell receptor (dTCR) polypeptide pair, or a single chain T-cell receptor (scTCR) polypeptide wherein

the dTCR polypeptide pair is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains, and the scTCR is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain;

the variable region sequences of the dTCR polypeptide pair or scTCR polypeptide are mutually orientated substantially as in native TCRs; and

in the case of the scTCR polypeptide a disulfide bond which has no equivalent in native T cell receptors links residues of the polypeptide.

In the case of αβ scTCRs or dTCRs displayed according to the invention, the requirement that the variable region sequences of the α and β segments are mutually orientated substantially as in native αβ T cell receptors is tested by confirming that the molecule binds to the relevant TCR ligand (pMHC complex, CD1-antigen complex, superantigen or superantigen/pMHC complex) - if it binds, then the requirement is met. Interactions with pMHC complexes can be measured using a BIAcore 3000™ or

BIAcore 2000™ instrument. WO99/6120 provides detailed descriptions of the methods required to analyse TCR binding to MHC-peptide complexes. These methods are equally applicable to the study of TCR/ CD1 and TCR/superantigen interactions. In order to apply these methods to the study of TCR/CD1 interactions soluble forms of CD1 are required, the production of which are described in (Bauer (1997) Eur J Immunol 27 (6) 1366-1373). In the case of γδ TCRs of the present invention the cognate ligands for these molecules are unknown therefore secondary means of verifying their conformation such as recognition by antibodies can be employed. The monoclonal antibody MCA991T (available from Serotec), specific for the δ chain variable region, is an example of an antibody appropriate for this task.

The scTCRs or dTCRs of the present invention may be displayed on phage particles by, for example, the following two means:

(i) The C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, can be directly linked by a peptide bond to a surface exposed residue of the proteinaceous particle. For example, the said surface exposed residue is preferably at the N-terminus of the gene product of bacteriophage gene III or gene VIII; and

(ii) The C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a disulfide bond to a surface exposed cysteine residue of the proteinaceous particle via an introduced cysteine residue. For example, the said surface exposed residue is again preferably at the N-terminus of the gene product of bacteriophage gene III or gene VIII.

Method (i) above is preferred. In the case of a scTCR, nucleic acid encoding the TCR may be fused to nucleic acid encoding the particle forming protein or a surface protein of the replicable particle such as a phage. Alternatively, nucleic acid representing mRNA but without a stop codon, or fused to puromycin RNA may be translated by ribosome such that the TCR remains fused to the ribosome particle. In the case of a

dTCR, nucleic acid encoding one chain of the TCR may be fused tonucleic acid encoding the particle forming protein or a surface protein of the replicable particle such as a phage, and the second chain of the TCR polypeptide pair may be allowed to associate with the resultant expressed particle displaying the first chain. Proper functional association of the two chains is assisted by the presence of cysteines in the constant region of the two chains which are capable of forming an interchain disulfide bond, as more fully discussed below.

The displayed scTCR

The displayed scTCR polypeptide may be, for example, one which has

a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence,

a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region fused to the N terminus of an amino acid sequence corresponding to TCR β chain constant region extracellular sequence,

a linker sequence linking the C terminus of the first segment to the N terminus of the second segment, or vice versa, and

a disulfide bond between the first and second chains, said disulfide bond being one which has no equivalent in native αβ or γδ T cell receptors,

the length of the linker sequence and the position of the disulfide bond being such that the variable region sequences of the first and second segments are mutually orientated substantially as in native αβ or γδ T cell receptors.

The displayed dTCR

The dTCR which is displayed on the proteinaceous particle may be one which is constituted by

a first polypeptide wherein a sequence corresponding to a TCR α or δ chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant region extracellular sequence, and

a second polypeptide wherein a sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus a sequence corresponding to a TCR β chain constant region extracellular sequence,

the first and second polypeptides being linked by a disulfide bond which has no equivalent in native αβ or γδ T cell receptors.

dTCR Polypeptide Pair and scTCR Polypeptide

The constant region extracellular sequences present in the scTCRs or dTCRs preferably correspond to those of a human TCR, as do the variable region sequences. However, the correspondence between such sequences need not be 1:1 on an amino acid level. N- or C-truncation, and/or amino acid deletion and/or substitution relative to the corresponding human TCR sequences is acceptable, provided the overall result is mutual orientation of the α and β variable region sequences, or γ and δ variable region sequences is as in native αβ, or γδ T cell receptors respectively. In particular, because the constant region extracellular sequences present in the first and second segments are not directly involved in contacts with the ligand to which the scTCR or dTCR binds, they may be shorter than, or may contain substitutions or deletions relative to, extracellular constant domain sequences of native TCRs.

The constant region extracellular sequence present in one of the dTCR polypeptide pair, or in the first segment of a scTCR polypeptide may include a sequence

corresponding to the extracellular constant Ig domain of a TCR α chain, and/or the constant region extracellular sequence present in the other member of the pair or second segment may include a sequence corresponding to the extracellular constant Ig domain of a TCR β chain.

In one embodiment of the invention, one member of the polypeptide pair or the first segment of the scTCR polypeptide corresponds to substantially all the variable region of a TCR α chain fused to the N terminus of substantially all the extracellular domain of the constant region of an TCR α chain; and/or the other member of the pair or second segment corresponds to substantially all the variable region of a TCR β chain fused to the N terminus of substantially all the extracellular domain of the constant region of a TCR β chain.

In another embodiment, the constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide correspond to the constant regions of the α and β chains of a native TCR truncated at their C termini such that the cysteine residues which form the native inter-chain disulfide bond of the TCR are excluded. Alternatively those cysteine residues may be substituted by another amino acid residue such as serine or alanine, so that the native disulfide bond is deleted. In addition, the native TCR β chain contains an unpaired cysteine residue and that residue may be deleted from, or replaced by a non-cysteine residue in, the β sequence of the scTCR of the invention.

In one particular embodiment of the invention, the TCR α and β chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may together correspond to the functional variable domain of a first TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a second TCR, the first and second TCRs being from the same species. Thus the α and β chain variable region sequences present in dTCR

polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second human TCR. For example, A6 Tax sTCR constant region extracellular sequences can be used as a framework onto which heterologous α and β variable domains can be fused.

In another embodiment of the invention, the TCR δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide respectively, may together correspond to the functional variable domain of a first TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide respectively, may correspond to those of a second TCR, the first and second TCRs being from the same species. Thus the δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second human TCR. For example, A6 Tax sTCR constant region extracellular sequences can be used as a framework onto which heterologous γ and δ variable domains can be fused.

In one particular embodiment of the invention, the TCR α and β, or δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may together correspond to the functional variable domain of a first human TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a second non-human TCR, Thus the α and β, or δ and γ chain variable region sequences present dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second non-human TCR. For example, murine TCR constant

region extracellular sequences can be used as a framework onto which heterologous human α and β TCR variable domains can be fused.

Linker in the scTCR Polypeptide

For scTCR-displaying proteinaceous particles of the present invention, a linker sequence links the first and second TCR segments, to form a single polypeptide strand. The linker sequence may, for example, have the formula -P-AA-P- wherein P is proline and AA represents an amino acid sequence wherein the amino acids are glycine and serine.

For the scTCR displayed by proteinaceous particles of the present invention to bind to a ligand, MHC-peptide complex in the case of αβ TCRs, the first and second segments must be paired so that the variable region sequences thereof are orientated for such binding. Hence the linker should have sufficient length to span the distance between the C terminus of the first segment and the N terminus of the second segment, or vice versa. On the other hand excessive linker length should preferably be avoided, in case the end of the linker at the N-terminal variable region sequence blocks or reduces bonding of the scTCR to the target ligand.

For example, in the case where the constant region extracellular sequences present in the first and second segments correspond to the constant regions of the α and β chains of a native TCR truncated at their C termini such that the cysteine residues which form the native interchain disulfide bond of the TCR are excluded, and the linker sequence links the C terminus of the first segment to the N terminus of the second segment, the linker may consist of from 26 to 41, for example 29, 30, 31 or 32 amino acids, and a particular linker has the formula -PGGG-$(SGGGG)_5$-P- wherein P is proline, G is glycine and S is serine.

Inter-chain Disulfide bond

A principle characterising feature of the scTCRs displayed by proteinaceous particles of the present invention, and preferably a feature of the displayed dTCRs, is ~~the~~ a

disulfide bond between the constant region extracellular sequences of the dTCR polypeptide pair or first and second segments of the scTCR polypeptide. That bond may correspond to the native inter-chain disulfide bond present in native dimeric αβ TCRs, or may have no counterpart in native TCRs, being between cysteines specifically incorporated into the constant region extracellular sequences of dTCR polypeptide pair or first and second segments of the scTCR polypeptide. In some cases, both a native and a non-native disulfide bond may be desirable.

The position of the disulfide bond is subject to the requirement that the variable region sequences of dTCR polypeptide pair or first and second segments of the scTCR polypeptide are mutually orientated substantially as in native αβ or γδ T cell receptors.

The disulfide bond may be formed by mutating non-cysteine residues on the first and second segments to cysteine, and causing the bond to be formed between the mutated residues. Residues whose respective β carbons are approximately 6 Å (0.6 nm) or less, and preferably in the range 3.5 Å (0.35 nm) to 5.9 Å (0.59 nm) apart in the native TCR are preferred, such that a disulfide bond can be formed between cysteine residues introduced in place of the native residues. It is preferred if the disulfide bond is between residues in the constant immunoglobulin region, although it could be between residues of the membrane proximal region. Preferred sites where cysteines can be introduced to form the disulfide bond are the following residues in exon 1 of TRAC*01 for the TCR α chain and TRBC1*01 or TRBC2*01 for the TCR β chain:

TCR α chain	TCR β chain	Native β carbon separation (nm)
Thr 48	Ser 57	0.473
Thr 45	Ser 77	0.533
Tyr 10	Ser 17	0.359
Thr 45	Asp 59	0.560
Ser 15	Glu 15	0.59

Now that the residues in human TCRs which can be mutated into cysteine residues to form a new interchain disulfide bond in dTCRs or scTCRs displayed according to the invention have been identified, those of skill in the art will be able to mutate TCRs of other species in the same way to produce a dTCR or scTCR of that species for phage display. In humans, the skilled person merely needs to look for the following motifs in the respective TCR chains to identify the residue to be mutated (the shaded residue is the residue for mutation to a cysteine).

α Chain Thr 48: DSDVYITDKTVLDMRSMDFK (amino acids 39-58 of exon 1 of the TRAC*01 gene)

α Chain Thr 45: QSKDSDVYITDKTVLDMRSM(amino acids 36-55 of exon 1 of the TRAC*01 gene)

α Chain Tyr 10: DIQNPDPAVYQLRDSKSSDK(amino acids 1-20 of exon 1 of the TRAC*01 gene)

α Chain Ser 15: DPAVYQLRDSKSSDKSVCLF(amino acids 6-25 of exon 1 of the TRAC*01 gene)

β Chain Ser 57: NGKEVHSGVSTDPQPLKEQP(amino acids 48- 67 of exon 1 of the TRBC1*01 & TRBC2*01 genes)

β Chain Ser 77: ALNDSRYALSSRLRVSATFW(amino acids 68- 87 of exon 1 of the TRBC1*01 & TRBC2*01 genes)

β Chain Ser 17: PPEVAVFEPSEAEISHTQKA(amino acids 8- 27 of exon 1 of the TRBC1*01 & TRBC2*01 genes)

β Chain Asp 59: KEVHSGVSTDPQPLKEQPAL(amino acids 50- 69 of exon 1 of the TRBC1*01 & TRBC2*01 genes gene)

β Chain Glu 15: VFPPEVAVFEPSEAEISHTQ(amino acids 6- 25 of exon 1 of the TRBC1*01 & TRBC2*01 genes)

In other species, the TCR chains may not have a region which has 100% identity to the above motifs. However, those of skill in the art will be able to use the above motifs to identify the equivalent part of the TCR α or β chain and hence the residue to be mutated to cysteine. Alignment techniques may be used in this respect. For example, ClustalW, available on the European Bioinformatics Institute website (http://www.ebi.ac.uk/index.html) can be used to compare the motifs above to a particular TCR chain sequence in order to locate the relevant part of the TCR sequence for mutation.

The present invention includes within its scope proteinaceous particle-displayed αβ and γδ-analogue scTCRs, as well as those of other mammals, including, but not limited to, mouse, rat, pig, goat and sheep. As mentioned above, those of skill in the art will be able to determine sites equivalent to the above-described human sites at which cysteine residues can be introduced to form an inter-chain disulfide bond. For example, the following shows the amino acid sequences of the mouse Cα and Cβ soluble domains, together with motifs showing the murine residues equivalent to the human residues mentioned above that can be mutated to cysteines to form a TCR interchain disulfide bond (where the relevant residues are shaded):

Mouse Cα soluble domain:

PYIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDMK
AMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP

Mouse Cβ soluble domain:

EDLRNVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGREV
HSGVSTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK
WPEGSPKPVTQNISAEAWGRAD

Murine equivalent of human α Chain Thr 48: ESGTFITDKTVLDMKAMDSK

Murine equivalent of human α Chain Thr 45: KTMESGTFITDKTVLDMKAM

Murine equivalent of human α Chain Tyr 10: YIQNPEPAVYQLKDPRSQDS

Murine equivalent of human α Chain Ser 15: AVYQLKDPRSQDSTLCLFTD

Murine equivalent of human β Chain Ser 57: NGREVHSGVSTDPQAYKESN

Murine equivalent of human β Chain Ser 77: KESNYSYCLSSRLRVSATFW

Murine equivalent of human β Chain Ser 17: PPKVSLFEPSKAEIANKQKA

Murine equivalent of human β Chain Asp 59: REVHSGVSTDPQAYKESNYS

Murine equivalent of human β Chain Glu 15: VTPPKVSLFEPSKAEIANKQ

As discussed above, the A6 Tax sTCR extracellular constant regions can be used as framework onto which heterologous variable domains can be fused. It is preferred that the heterologous variable region sequences are linked to the constant region sequences at any point between the disulfide bond and the N termini of the constant region sequences. In the case of the A6 Tax TCR α and β constant region sequences, the disulfide bond may be formed between cysteine residues introduced at amino acid residues 158 and 172 respectively. Therefore it is preferred if the heterologous α and β chain variable region sequence attachment points are between residues 159 or 173 and the N terminus of the α or β constant region sequences respectively.

TCR Display.

The preferred *in-vivo* TCR display method for biopanning to identify TCRs having desirable properties such as strong affinity for a target peptide-MHC complex is phage display.

Firstly, a DNA library is constructed that encodes a diverse array of mutated scTCRs or dTCRs. This library is constructed by using DNA encoding a native TCR as the template for amplification. There are a number of suitable methods, known to those skilled in the art, for the introduction of the desired mutations into the TCR DNA, and hence the finally expressed TCR protein. For example error-prone PCR (EP-TCR), DNA shuffling techniques, and the use of bacterial mutator strains such as XL-1-Red are convenient means of introducing mutations into the TCR sequences. It is particularly preferred if these mutations are introduced into defined regions of the TCRs. For example, mutations in the variable region, particularly the complementarity-determining regions (CDRs) are likely to be the most appropriate sites for the introduction of mutations leading to the production of a diverse library of TCRs for the production of TCRs with enhanced ligand-binding properties. EP-PCR is an example of a method by which such 'region-specific' mutations can be introduced into the TCRs. EP-PCR primers are used that are complementary to DNA sequences bordering the region to be mutated to amplify multiple copies of this region of the TCR DNA that contain a controllable level of random mutations. These DNA sequences encoding mutated regions are inserted into the DNA sequences, which encode the non-mutagenised sections of the TCR, by ligation or overlapping PCR. The DNA encoding the TCR with mutated region can then be ligated onto DNA encoding a heterologous polypeptide in order to produce a fusion protein suitable for display. In the case of phage-display the expression vector utilised is either a phagemid or a phage gemone vector in which the TCR DNA can be ligated to DNA encoding the gIII or gVIII surface protein. In the case of a scTCR such ligation is performed as for phage display of any monomeric peptide or polypeptide. In the case of dTCRs, only one of the TCR chains is ligated as aforesaid. The other chain is

encoded in nucleic acid for co-expression with the phagemid and helper phage nucleic acid, so that the expressed second chain finds and associates with the expressed phage with surface displayed first chain. In both cases, as discussed in more detail above, properly positioned cysteines in the constant regions are helpful in causing the variable regions of the TCR to adopt their functional positions, through the formation of a disulfide bond by those cysteines.

For expression, the expression vectors comprising the TCR DNA library are then contacted with host cells capable of causing the expression of the encoded genetic material under conditions suitable to allow the transformation of said cells. Such expression vectors and host cells harbouring them from additional aspects of the current invention.

The transformed cells are then incubated to allow the expression of the TCR-displaying proteinaceous particles. These particles can then be used for screening or in assays to identify TCR variants with specific enhanced characteristics. Any particles that possess the enhanced characteristics under investigation can then be isolated. The DNA encoding these TCRs can then be amplified by PCR and the sequence determined.

It is known that high expression levels of an exogenous polypeptide may be toxic to the host cell. In such cases, either a host strain which is more tolerant of the exogenous polypeptide must be found, or the expression levels in the host cell must be limited to a level which is tolerated. For example (Beekwilder *et al.*, (1999) Gene *228* (1-2) 23-31) report that only mutated forms of a potato protease inhibitor (PI2) which contained deletions or amber stop codons would be successfully selected from a phage display library. In the present case, an observation in the course of the work reported in the Examples herein suggests that it may be desirable to limit the expression levels of protein particle-displayed TCRs of the invention, at least in some strains of *E. coli.* Thus, the A6 TCR selected in Example 4 after repeated rounds of culture was shown to be derived from cells in which the phagemid had mutated relative to that introduced

at the start. The mutation had created an 'opal' stop codon in the TCR β chain. This codon is 'read-through' with low frequency by ribosomes of the *E.coli* strain utilised resulting in the insertion of a tryptophan residue at this site and a much reduced overall level of full-length β chain expression.

There are several strategies for limiting the expression levels of an exogenous polypeptide from a given expression vector in a host which may be suitable for the limiting the expression levels of a scTCR, or one, or both TCR chains of a dTCR . For example:

Use of a weak promoter sequence – The level of expression obtained for a given gene product, such as the TCR α or β chain, can be tailored by using promoter sequences of varying strengths. The lambda phage P_{RM} promoter is an example of a weak promoter.

Mutated ribosome binding sites (RBS's) – Mutating a single nucleic acid in the RBS associated with a gene product, such as the TCR α or β chain, can result in a reduced level of expression. For example, mutating a wild-type AGGA sequence to AGGG.

Mutated 'start codons' - Mutating a single nucleic acid in the start codon associated with a gene product, such as the TCR α or β chain, can also result in a reduced level of expression. For example, mutating a wild-type AUG start codon to GUG.

Miss-sense suppressor mutations – These are inserted within the TCR β chain coding regions. Examples include the 'opal' stop codon (UGA), this 'leaky' stop codon results in the low frequency insertion of a tryptophan amino acid and read-through of the rest of the coding sequence.

Metabolite-mediated modification of promoter strength – The level of expression of a gene product, such as the TCR α or β chain, under the control of certain promoters can be down-regulated by the addition of a relevant metabolite to the cells containing the

promoter. For example, glucose additions can be used to down-regulate expression of a gene product under the control of a Lac promoter.

Codon usage - Bacterial cells and, for example, mammalian cells have different 'preferences' relating to the codons they use to encode certain amino acids. For example, bacterial cells most commonly use the CGU codon to encode arginine whereas eucaryotic cells most commonly use AGA. It is possible to reduce the level of expression of a gene product, such as the TCR α or β chain, by utilising DNA sequences that contain a number of codons less preferred by the expression system being utilised.

Details relating to the above means of down-regulating gene product expression can be found in (Glass (1982) Gene Function – *E.coli* and its heritable elements, Croom Helm) and (Rezinoff (1980) The Operon 2nd Edition, Cold Spring Harbor Laboratory).

It is also known that supplying bacterial cultures with a relatively high concentration of a sugar such as sucrose can increase periplasmic expression levels of soluble proteins. (See for example (Sawyer *et al.*, (1994) Protein Engineering 7 **(11)** 1401-1406))

As mentioned above, for scTCR phage display, the scTCR polypeptide is expressed according to any of the three general prior art techniques discussed earlier as Methods A, B, and C. For the scTCRs displayed by phage particles of the present invention to bind to a ligand, MHC-peptide complex in the case of αβ TCRs, the first and second segments must be paired so that the variable region sequences thereof are orientated for such binding. This correct pairing is assisted by the introduction of a disulfide bond in the extracellular constant region of the scTCR. Without wanting to be limited by theory, the novel disulfide bond is believed to provide extra stability to the scTCR during the folding process and thereby facilitating correct pairing of the first and second segments.

Also as mentioned above, for dTCR phage display, one of the dTCR polypeptide pair is expressed according to any of the three general prior art techniques discussed earlier as Methods A, B, and C as if it were eventually to be displayed as a monomeric polypeptide on the phage, and the other of the dTCR polypeptide pair is co-expressed in the same host cell. As the phage particle self assembles, the two polypeptides self associate for display as a dimer on the phage. Again, in the preferred embodiment of this aspect of the invention, correct folding during association of the polypeptide pair is assisted by a disulfide bond between the constant sequences, as discussed above. Further details of a procedure for phage display of a dTCR having an interchain disulfide bond appear in the Examples herein.

As an alternative, the phage displaying the first chain of the TCR may be expressed first, and the second chain polypeptide may be contacted with the expressed phage in a subsequent step, for association as a functional TCR on the phage surface.

The preferred *in-vitro* TCR display method for biopanning to identify TCRs having desirable properties such as strong affinity for a target peptide-MHC complex is ribosomal display of scTCRs.

Firstly, a DNA library is constructed that encodes a diverse array of mutated TCRs using the techniques discussed above.

The DNA library is then contacted with RNA polymerase in order to produce a complementary mRNA library. Optionally, for mRNA display techniques the mRNA sequences can then be ligated to a DNA sequence comprising a puromycin binding site. These genetic constructs are then contacted with ribosomes in-vitro under conditions allowing the translation of the scTCR polypeptide. These scTCR-displaying ribosomes can then used for screening or in assays to identify TCR variants with specific enhanced characteristics. Any particles that possess the enhanced characteristics under investigation can then be isolated. The mRNA encoding these TCRs can then converted to the complementary DNA sequences using reverse transcriptase. This DNA can then be amplified by PCR and the sequence determined.

Additional Aspects

A proteinaceous particle displaying a scTCR or dTCR (which preferably is constituted by constant and variable sequences corresponding to human sequences) of the present invention may be provided in substantially pure form, or as a purified or isolated preparation. For example, it may be provided in a form which is substantially free of other proteins.

A phage particle displaying a plurality of scTCRs or dTCRs of the present invention may be provided in a multivalent complex. Thus, the present invention provides, in one aspect, a multivalent T cell receptor (TCR) complex, which comprises a phage particle displaying a plurality of scTCRs or dTCRs as described herein. Each of the plurality of said scTCRs or dTCRs is preferably identical.

In a further aspect, the invention provides a method for detecting TCR ligand complexes, which comprises:

a. providing a TCR-displaying proteineaceous particle of the current invention
b. contacting the TCR-displaying phage with the putative ligand complexes; and
detecting binding of the TCR-displaying proteinaceous particle to the putative ligand complexes.

TCR ligands suitable for identification by the above method include, but are not limited to, peptide-MHC complexes.

Isolation of TCR variants with enhanced characteristics

A further aspect of the invention is a method for the isolation of TCRs with a specific enhanced characteristic, said method comprising subjecting a diverse library of TCRs displayed on proteinaceous particles to an assay which measures said characteristic and thereby identifying those proteinaceous particles which display a TCR with the

desired enhancement and isolating these proteinaceous particles. The DNA sequences encoding the variant TCRs can then be obtained and amplified by PCR to allow the sequences to be determined. The characteristics that can be enhanced include, but are not limited to, ligand binding affinity and construct stability.

Screening Use

The TCR-displaying proteinaceous particles of the present invention are capable of utilisation in screening methods designed to identify modulators, including inhibitors, of the TCR-mediated cellular immune synapse.

As is know to those skilled in the art there are a number of assay formats that provide a suitable basis for protein-protein interaction screens of this type.

Amplified Luminescent Proximity Homogeneous Assay systems such as the AlphaScreen™, rely on the use of "Donor" and "Acceptor" beads that are coated with a layer of hydrogel to which receptor and ligand proteins can be attached. The interaction between these receptor and ligand molecules brings the beads into proximity. When these beads are subject to laser light a photosensitizer in the "Donor" bead converts ambient oxygen to a more excited singlet state. The singlet state oxygen molecules diffuse across to react with a chemiluminescer in the "Acceptor" bead that further activates fluorophores contained within the same bead. The fluorophores subsequently emit light at 520-620 nm, this signals that the receptor-ligand interaction has occurred. The presence of an inhibitor of the receptor-ligand interaction causes this signal to be diminished.

Surface Plasmon Resonance (SPR) is an interfacial optical assay, in which one binding partner (normally the receptor) is immobilised on a 'chip' (the sensor surface) and the binding of the other binding partner (normally the ligand), which is soluble and is caused to flow over the chip, is detected. The binding of the ligand results in an increase in concentration of protein near to the chip surface which causes a change in the refractive index in that region. The surface of the chip is comprised such that the

change in refractive index may be detected by surface plasmon resonance, an optical phenomenon whereby light at a certain angle of incidence on a thin metal film produces a reflected beam of reduced intensity due to the resonant excitation of waves of oscillating surface charge density (surface plasmons). The resonance is very sensitive to changes in the refractive index on the far side of the metal film, and it is this signal which is used to detect binding between the immobilised and soluble proteins. Systems which allow convenient use of SPR detection of molecular interactions, and data analysis, are commercially available. Examples are the Iasys™ machines (Fisons) and the Biacore™ machines.

Other interfacial optical assays include total internal reflectance fluorescence (TIRF), resonant mirror (RM) and optical grating coupler sensor (GCS), and are discussed in more detail in Woodbury and Venton (*J. Chromatog. B.* **725** 113-137 (1999)).

The scintillation proximity assay (SPA) has been used to screen compound libraries for inhibitors of the low affinity interaction between CD28 and B7 (K_d probably in the region of 4 μM (Van der Merwe *et al* J. Exp. Med. **185**:393-403 (1997), Jenh *et al,* Anal Biochem **165**(2) 287-93 (1998)). SPA is a radioactive assay making use of beta particle emission from certain radioactive isotopes which transfers energy to a scintillant immobilised on the indicator surface. The short range of the beta particles in solution ensures that scintillation only occurs when the beta particles are emitted in close proximity to the scintillant. When applied for the detection of protein-protein interactions, one interaction partner is labelled with the radioisotope, while the other is either bound to beads containing scintillant or coated on a surface together with scintillant. If the assay can be set up optimally, the radioisotope will be brought close enough to the scintillant for photon emission to be activated only when binding between the two proteins occurs.

A further aspect of the invention is a method of identifying an inhibitor of the interaction between a TCR-displaying proteinaceous particle of the invention, and a TCR-binding ligand comprising contacting the TCR-displaying proteinaceous particle with a TCR-binding ligand, in the presence of and in the absence of a test compound,

and determining whether the presence of the test compound reduces binding of the TCR-displaying proteinaceous particle to the TCR-binding ligand, such reduction being taken as identifying an inhibitor.

A further aspect of the invention is a method of identifying a potential inhibitor of the interaction between an TCR-displaying proteinaceous particle of the invention, and a TCR-binding ligand, for example a MHC-peptide complex, comprising contacting the TCR-displaying proteinaceous particle or TCR-binding ligand partner with a test compound and determining whether the test compound binds to the TCR-displaying proteinaceous particle and/or the TCR-binding ligand, such binding being taken as identifying a potential inhibitor. This aspect of the invention may find particular utility in interfacial optical assays such as those carried out using the BIAcore™ system.

High Affinity TCRs

The present invention also makes available mutated TCRs specific for a given TCR ligand with higher affinity for said TCR ligand than the wild-type TCR. These high affinity TCRs are expected to be particularly useful for the diagnosis and treatment of disease.

Where used herein the term 'high affinity TCR' is defined as as any mutated sc or dTCR of the present invention which interacts with a specific TCR ligand and either:

has a Kd for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

Or

has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

High affinity scTCRs or dTCRs of the present invention are preferably mutated relative to the native TCR in at least one complementarity determining region.

In one aspect of the present invention the TCR ligand for which a given high affinity TCR is specific is a pMHC.

In a further aspect of the present invention the TCR ligand for which a given high affinity TCR is specific is the HLA-A2 tax peptide (LLFGYPVYV) complex.

One or both of the high affinity TCR chains may be labelled with a detectable label, for example a label that is suitable for diagnostic purposes. Thus, the invention provides a method for detecting a TCR ligand selected from CD1-antigen complexes, bacterial superantigens, and MHC-peptide/superantigen complexes which method comprises contacting the TCR ligand with a high affinity TCR or multimeric high affinity TCR complex in accordance with the invention which is specific for the TCR ligand; and detecting binding of the high affinity TCR or multimeric high affinity TCR complex to the TCR ligand. In tetrameric high affinity TCR complexes formed using biotinylated heterodimers, fluorescent streptavidin (commercially available) can be used to provide a detectable label. A fluorescently-labelled tetramer is suitable for use in FACS analysis, for example to detect antigen presenting cells carrying the peptide for which the high affinity TCR is specific.

Another manner in which the soluble high affinity TCRs of the present invention may be detected is by the use of TCR-specific antibodies, in particular monoclonal antibodies. There are many commercially available anti-TCR antibodies, such as αFl and βFl, which recognise the constant regions of the α and β chain, respectively.

The high affinity TCR (or multivalent complex thereof) of the present invention may alternatively or additionally be associated with (e.g. covalently or otherwise linked to) a therapeutic agent which may be, for example, a toxic moiety for use in cell killing, or an immunostimulating agent such as an interleukin or a cytokine. A multivalent

high affinity TCR complex of the present invention may have enhanced binding capability for a TCR ligand compared to a non-multimeric wild-type or high affinity T cell receptor heterodimer. Thus, the multivalent high affinity TCR complexes according to the invention are particularly useful for tracking or targeting cells presenting particular antigens *in vitro* or *in vivo*, and are also useful as intermediates for the production of further multivalent high affinity TCR complexes having such uses. The high affinity TCR or multivalent high affinity TCR complex may therefore be provided in a pharmaceutically acceptable formulation for use *in vivo*.

The invention also provides a method for delivering a therapeutic agent to a target cell, which method comprises contacting potential target cells with a high affinity TCR or multivalent high affinity TCR complex in accordance with the invention under conditions to allow attachment of the high affinity TCR or multivalent high affinity TCR complex to the target cell, said high affinity TCR or multivalent high affinity TCR complex being specific for the TCR ligand and having the therapeutic agent associated therewith.

In particular, the soluble high affinity TCR or multivalent high affinityTCR complex can be used to deliver therapeutic agents to the location of cells presenting a particular antigen. This would be useful in many situations and, in particular, against tumours. A therapeutic agent could be delivered such that it would exercise its effect locally but not only on the cell it binds to. Thus, one particular strategy envisages anti-tumour molecules linked to high affinity T cell receptors or multivalent high affinity TCR complexes specific for tumour antigens.

Many therapeutic agents could be employed for this use, for instance radioactive compounds, enzymes (perforin for example) or chemotherapeutic agents (cis-platin for example). To ensure that toxic effects are exercised in the desired location the toxin could be inside a liposome linked to streptavidin so that the compound is released slowly. This will prevent damaging effects during the transport in the body and ensure

that the toxin has maximum effect after binding of the TCR to the relevant antigen presenting cells.

Other suitable therapeutic agents include:

- small molecule cytotoxic agents, i.e. compounds with the ability to kill mammalian cells having a molecular weight of less than 700 daltons. Such compounds could also contain toxic metals capable of having a cytotoxic effect. Furthermore, it is to be understood that these small molecule cytotoxic agents also include pro-drugs, i.e. compounds that decay or are converted under physiological conditions to release cytotoxic agents. Examples of such agents include cis-platin, maytansine derivatives, rachelmycin, calicheamicin, docetaxel, etoposide, gemcitabine, ifosfamide, irinotecan, melphalan, mitoxantrone, sorfimer sodiumphotofrin II, temozolmide, topotecan, trimetreate glucuronate, auristatin E vincristine and doxorubicin;
- peptide cytotoxins, i.e. proteins or fragments thereof with the ability to kill mammalian cells. Examples include ricin, diphtheria toxin, pseudomonas bacterial exotoxin A, DNAase and RNAase;
- radio-nuclides, i.e. unstable isotopes of elements which decay with the concurrent emission of one or more of α or β particles, or γ rays. Examples include iodine 131, rhenium 186, indium 111, yttrium 90, bismuth 210 and 213, actinium 225 and astatine 213; chelating agents may be used to facilitate the association of these radio-nuclides to the high affinity TCRs, or multimers thereof;
- prodrugs, such as antibody directed enzyme pro-drugs;
- immuno-stimulants, i.e. moieties which stimulate immune response. Examples include cytokines such as IL-2, chemokines such as IL-8, platelet factor 4, melanoma growth stimulatory protein, etc, antibodies or fragments thereof, complement activators, xenogeneic protein domains, allogeneic protein domains, viral/bacterial protein domains and viral/bacterial peptides.

Soluble high affinity TCRs or multivalent high affinity TCR complexes of the invention may be linked to an enzyme capable of converting a prodrug to a drug. This

allows the prodrug to be converted to the drug only at the site where it is required (i.e. targeted by the sTCR).

A multitude of disease treatments can potentially be enhanced by localising the drug through the specificity of soluble high affinity TCRs. For example, it is expected that the high affinity HLA-A2-tax (LLFGYPVYV) specific A6 TCR disclosed herein may be used in methods for the diagnosis and treatment of HTLV-1.

Viral diseases for which drugs exist, e.g. HIV, SIV, EBV, CMV, would benefit from the drug being released or activated in the near vicinity of infected cells. For cancer, the localisation in the vicinity of tumours or metastasis would enhance the effect of toxins or immunostimulants. In autoimmune diseases, immunosuppressive drugs could be released slowly, having more local effect over a longer time-span while minimally affecting the overall immuno-capacity of the subject. In the prevention of graft rejection, the effect of immunosuppressive drugs could be optimised in the same way. For vaccine delivery, the vaccine antigen could be localised in the vicinity of antigen presenting cells, thus enhancing the efficacy of the antigen. The method can also be applied for imaging purposes.

The soluble high affinity TCRs of the present invention may be used to modulate T cell activation by binding to specific TCR ligand and thereby inhibiting T cell activation. Autoimmune diseases involving T cell-mediated inflammation and/or tissue damage would be amenable to this approach, for example type I diabetes. Knowledge of the specific peptide epitope presented by the relevant pMHC is required for this use.

Medicaments in accordance with the invention will usually be supplied as part of a sterile, pharmaceutical composition which will normally include a pharmaceutically acceptable carrier. This pharmaceutical composition may be in any suitable form, (depending upon the desired method of administering it to a patient). It may be provided in unit dosage form, will generally be provided in a sealed container and may be provided

as part of a kit. Such a kit would normally (although not necessarily) include instructions for use. It may include a plurality of said unit dosage forms.

The pharmaceutical composition may be adapted for administration by any appropriate route, for example by the oral (including buccal or sublingual), rectal, nasal, topical (including buccal, sublingual or transdermal), vaginal or parenteral (including subcutaneous, intramuscular, intravenous or intradermal) route. Such compositions may be prepared by any method known in the art of pharmacy, for example by admixing the active ingredient with the carrier(s) or excipient(s) under sterile conditions.

Pharmaceutical compositions adapted for oral administration may be presented as discrete units such as capsules or tablets; as powders or granules; as solutions, syrups or suspensions (in aqueous or non-aqueous liquids; or as edible foams or whips; or as emulsions). Suitable excipients for tablets or hard gelatine capsules include lactose, maize starch or derivatives thereof, stearic acid or salts thereof. Suitable excipients for use with soft gelatine capsules include for example vegetable oils, waxes, fats, semi-solid, or liquid polyols etc.

For the preparation of solutions and syrups, excipients which may be used include for example water, polyols and sugars. For the preparation of suspensions oils (e.g. vegetable oils) may be used to provide oil-in-water or water in oil suspensions. Pharmaceutical compositions adapted for transdermal administration may be presented as discrete patches intended to remain in intimate contact with the epidermis of the recipient for a prolonged period of time. For example, the active ingredient may be delivered from the patch by iontophoresis as generally described in *Pharmaceutical Research*, 3(6):318 (1986). Pharmaceutical compositions adapted for topical administration may be formulated as ointments, creams, suspensions, lotions, powders, solutions, pastes, gels, sprays, aerosols or oils. For infections of the eye or other external tissues, for example mouth and skin, the compositions are preferably applied as a topical ointment or cream. When formulated in an ointment, the active ingredient may be employed with either a paraffinic or a water-miscible ointment base. Alternatively, the active ingredient may be

formulated in a cream with an oil-in-water cream base or a water-in-oil base. Pharmaceutical compositions adapted for topical administration to the eye include eye drops wherein the active ingredient is dissolved or suspended in a suitable carrier, especially an aqueous solvent. Pharmaceutical compositions adapted for topical administration in the mouth include lozenges, pastilles and mouth washes.

Pharmaceutical compositions adapted for rectal administration may be presented as suppositories or enemas. Pharmaceutical compositions adapted for nasal administration wherein the carrier is a solid include a coarse powder having a particle size for example in the range 20 to 500 microns which is administered in the manner in which snuff is taken, i.e. by rapid inhalation through the nasal passage from a container of the powder held close up to the nose. Suitable compositions wherein the carrier is a liquid, for administration as a nasal spray or as nasal drops, include aqueous or oil solutions of the active ingredient. Pharmaceutical compositions adapted for administration by inhalation include fine particle dusts or mists which may be generated by means of various types of metered dose pressurised aerosols, nebulizers or insufflators. Pharmaceutical compositions adapted for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray formulations. Pharmaceutical compositions adapted for parenteral administration include aqueous and non-aqueous sterile injection solution which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation substantially isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. Excipients which may be used for injectable solutions include water, alcohols, polyols, glycerine and vegetable oils, for example. The compositions may be presented in unit-dose or multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carried, for example water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets.

The pharmaceutical compositions may contain preserving agents, solubilising agents, stabilising agents, wetting agents, emulsifiers, sweeteners, colourants, odourants, salts (substances of the present invention may themselves be provided in the form of a pharmaceutically acceptable salt), buffers, coating agents or antioxidants. They may also contain therapeutically active agents in addition to the substance of the present invention.

Dosages of the substances of the present invention can vary between wide limits, depending upon the disease or disorder to be treated, the age and condition of the individual to be treated, etc. and a physician will ultimately determine appropriate dosages to be used. The dosage may be repeated as often as appropriate. If side effects develop the amount and/or frequency of the dosage can be reduced, in accordance with normal clinical practice.

The invention also provides a method for obtaining a high affinity TCR chain, which method comprises incubating such a host cell under conditions causing expression of the high affinity TCR chain and then purifying the polypeptide.

Preferred features of each aspect of the invention are as for each of the other aspects *mutatis mutandis*. The prior art documents mentioned herein are incorporated to the fullest extent permitted by law.

Examples

The invention is further described in the following examples, which do not limit the scope of the invention in any way.

Reference is made in the following to the accompanying drawings in which:

Figures 1a and 1b show respectively the nucleic acid sequences of a soluble A6 TCR α and β chains, mutated so as to introduce a cysteine codon. The shading indicates the introduced cysteine codons.

Figure 2a shows the A6 TCR α chain extracellular amino acid sequence, including the $T_{48} \rightarrow C$ mutation (underlined) used to produce the novel disulphide inter-chain bond, and Figure 2b shows the A6 TCR β chain extracellular amino acid sequence, including the $S_{57} \rightarrow C$ mutation (underlined) used to produce the novel disulphide inter-chain bond.

Figure 3 Outlines the cloning of TCR α and β chains into phagemid vectors. The diagram describes a phage display vector. RSB is the ribosome-binding site. S1 or S2 are signal peptides for secretion of proteins into periplasm of *E. coli*. The * indicates translation stop codon. Either of the TCR α chain or β chain can be fused to phage coat protein, however in this diagram only TCR β chain is fused to phage coat protein.

Figure 4 details the DNA sequence of phagemid pEX746:A6.

Figure 5 expression of phage particle fusions of bacterial coat protein and heterodimeric A6 TCR in *E. coli*. Fusion proteins of heterodimeric A6 TCR::gIII are detected using western blotting. Phage particles are prepared from *E. coli* XL-1-Blue and concentrated with PEG/NaCl. The samples are loaded in reducing or non-reducing sample buffers. Lane 1 is the sample of clone 7 containing correct sequence, and lane 2 is the sample of clone 14 containing a deletion in the α-chain encoding gene. The heterodimeric A6 TCR:gIII fusion protein was detected at 125kDa.

Figure 6 illustrates ELISA detection of pMHC peptide complex binding activity of a heterodimeric A6 TCR displayed on phage. Clone 7 binds specifically to HLA A2-Tax complex. Clone 14 cannot bind to any pMHC, as no TCR is attached to the phage particles.

Figure 7a schematic illustration of the single-chain A6 TCR-C-Kappa DNA ribosome display construct.

Figure 7b details the complete DNA and amino acid sequences of the single-chain A6 TCR-C-Kappa DNA ribosome display construct encoded in pUC19.

Figure 8 details the DNA sequence of pUC19-T7.

Figure 9 details the DNA sequence of the single-chain A6 TCR-C-Kappa ribosome display construct that was cloned into pUC19-T7.

Figure 10 Western blot showing the detection of in-vitro translated single-chain A6 TCR-C-Kappa using Ambion rabbit reticulocyte lysates.

Figure 11 RT-PCR of the single–chain A6 TCR-C-Kappa mRNA on beads rescued from the ribosome display reactions.

Figure 12a details the DNA sequence of the A6 TCR Clone 9 mutated β chain; the mutated nucleic acid is indicated in bold.

Figure 12b details the amino acid sequence of the A6 TCR Clone 9 mutated β chain, the position corresponding to the introduced opal stop codon is indicated with an *.

Figure 13 details the DNA sequence of the A6 TCR Clone 49 mutated β chain; the mutated nucleic acid is indicated in bold. As this is a 'silent' mutation no change is introduced into the resulting amino acid sequence by this mutation.

Figure 14a details the DNA sequence of the A6 TCR Clone 134 mutated A6 TCR β chain; the mutated nucleic acids are indicated in bold.

Figure 14b details the amino acid sequence of the A6 TCR Clone 134 mutated A6 TCR β chain as tested by BIAcore assay; the mutated amino acids are indicated in bold.

Figure 14c details the amino acid sequence of the A6 TCR Clone 134 mutated A6 TCR β chain as tested by phage ELISA assay; the mutated amino acids are indicated in bold.

Figure 15 BIAcore data for the binding of A6 TCR clone 134 to HLA-A2 Tax and HLA-A2 NY-ESO

Figure 16 BIAcore data used to determine T_{OFF} for the binding of A6 TCR clone 134 to HLA-A2 Tax

Figures 17a and 17b show the DNA sequence of the mutated α and β chains of the NY-ESO TCR respectively

Figures 18a and 18b show the amino acid sequences of the mutated α and β chains of the NY-ESO TCR respectively

Figure 19 details the DNA and amino acid sequence of the NY-ESO TCR β chain as incorporated into the pEX746:NY-ESO phagemid respectively.

Figure 20 shows the specific binding of phage particles displaying the NY-ESO TCR to HLA-A2-NY-ESO in a phage ELISA assay.

Figure 21 shows the DNA sequence of the DR1α chain incorporating codons encoding the Fos dimerisation peptide attached to the 3' end of the DRA0101 sequence. Shading indicates the Fos codons and the biotinylation tag codons are indicated by in bold text.

Figure 22 shows the DNA sequence of the pAcAB3 bi-cistronic vector used for the expression of Class II HLA-peptide complexes in Sf9 insect cells. The Bgl II restriction site (AGATCT) used to insert the HLA α chain and the BamHI restriction site (GGATCC) used to insert the HLA β chain are indicated by shading.

Figure 23 shows the DNA sequence of the DR1 β chain incorporating codons encoding the Jun dimerisation peptide attached to the 3' end of the DRB0401

sequence and codons encoding an HLA-loaded peptide attached to the 5' end of the DRB0401 sequence. Shading indicates the Jun codons, and the HLA-loaded Flu HA peptide codons are underlined.

Figure 24 shows a BIAcore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

Flow-cell 2 (FC 2) - HLA-A2 (LLGRNSFEV)

Flow-cell 3 (FC 3) - HLA-A2 (KLVALGINAV)

Flow-cell 4 (FC 4) - HLA-A2 (LLGDLFGV)

Figure 25 shows a BIAcore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

Flow-cell 2 (FC 2) - HLA-B8 (FLRGRAYGL)

Flow-cell 3 (FC 3) - HLA-B27 (HRCQAIRKK)

Flow-cell 4 (FC 4) - HLA- Cw6 (YRSGIIAVV)

Figure 26 shows a BIAcore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) – Blank

Flow-cell 2 (FC 2) – HLA-A24 (VYGFVRACL)

Flow-cell 3 (FC 3) - HLA-A2 (ILAKFLHWL)

Flow-cell 4 (FC 4) - HLA-A2 (LTLGEFLKL)

Figure 27 shows a BIAcore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) – Blank

Flow-cell 2 (FC 2) – HLA-DR1 (PKYVKQNTLKLA)

Flow-cell 3 (FC 3) -HLA-A2 (GILGFVFTL)

Flow-cell 4 (FC 4) - HLA-A2 (SLYNTVATL)

Figure 28 shows a BIAcore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) – Blank

Flow-cell 4 (FC 4) - HLA-A2 (LLFGYPVYV)

Example 1 – Design of primers and mutagenesis of A6 Tax TCR α and β chains to introduce the cysteine residues required for the formation of a novel inter-chain disulphide bond

For mutating A6 Tax threonine 48 of exon 1 in TRAC*01 to cysteine, the following primers were designed (mutation shown in lower case):

5'-C ACA GAC AAA tgT GTG CTA GAC AT

5'-AT GTC TAG CAC Aca TTT GTC TGT G

For mutating A6 Tax serine 57 of exon 1 in both TRBC1*01 and TRBC2*01 to cysteine, the following primers were designed (mutation shown in lower case):

5'-C AGT GGG GTC tGC ACA GAC CC

5'-GG GTC TGT Gca GAC CCC ACT G

PCR mutagenesis:

Expression plasmids containing the genes for the A6 Tax TCR α or β chain were mutated using the α-chain primers or the β-chain primers respectively, as follows. 100 ng of plasmid was mixed with 5 µl 10 mM dNTP, 25 µl 10xPfu-buffer (Stratagene), 10 units Pfu polymerase (Stratagene) and the final volume was adjusted to 240 µl with H_2O. 48 µl of this mix was supplemented with primers diluted to give a final concentration of 0.2 µM in 50 µl final reaction volume. After an initial denaturation step of 30 seconds at 95°C, the reaction mixture was subjected to 15 rounds of denaturation (95°C, 30 sec.), annealing (55°C, 60 sec.), and elongation (73°C, 8 min.) in a Hybaid PCR express PCR machine. The product was then digested

for 5 hours at 37°C with 10 units of DpnI restriction enzyme (New England Biolabs). 10 µl of the digested reaction was transformed into competent XL1-Blue bacteria and grown for 18 hours at 37°C. A single colony was picked and grown over night in 5 ml TYP + ampicillin (16 g/l Bacto-Tryptone, 16 g/l Yeast Extract, 5 g/l NaCl, 2.5 g/l K_2HPO_4, 100 mg/l Ampicillin). Plasmid DNA was purified on a Qiagen mini-prep column according to the manufacturer's instructions and the sequence was verified by automated sequencing at the sequencing facility of Department of Biochemistry, Oxford University. The respective mutated nucleic acid and amino acid sequences are shown in Figures 1a and 2a for the α chain and Figures 1b and 2b for the β chain.

Example 2 – Construction of phage display vectors and cloning of A6 TCR α and β chains into the phagemid vectors.

In order to display a heterodimeric A6 TCR containing a non-native disulfide inter-chain bond on filamentous phage particles, phagemid vectors were constructed for expression of fusion proteins comprising the heterodimeric A6 TCR containing a non-native disulfide inter-chain bond with a phage coat protein. These vectors contain a pUC19 origin, an M13 origin, a bla (Ampicillin resistant) gene, Lac promoter/operator and a CAP-binding site. The design of these vectors is outlined in Figure 3, which describes vectors encoding for both the A6 TCR β chain-gp3 or A6 TCR β chain-gp8 fusion proteins in addition to the soluble A6 TCR α chain. The expression vectors containing the DNA sequences of the mutated A6 TCR α and β chains incorporating the additional cysteine residues required for the formation of a novel disulfide inter-chain bond prepared in Example 1 and as shown in figures 1a and 1b were used as the source of the A6 TCR α and β chains for the production of a phagemid encoding this TCR. The complete DNA sequence of the phagemid construct (pEX746) utilised is given in Figure 4.

The molecular cloning methods for constructing the vectors are described in "Molecular cloning: A laboratory manual, by J. Sambrook and D. W. Russell".

Primers listed in table-1 are used for construction of the vectors. A example of the PCR programme is 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 5 seconds, 53°C for 5 seconds and 72°C for 90 seconds, followed by 1 cycles of 72°C for 10 minutes, and then hold at 4°C. The Expand hifidelity Taq DNA polymerase is purchased from Roche.

Table 1. Primers used for construction of the A6 TCR phage display vectors

Primer name	Sequence 5' to 3'
YOL1	TAATAATACGTATAATAATATTCTATTTCAAG GAGACAGTC
YOL2	CAATCCAGCGGCTGCCGTAGGCAATAGGTATT TCATTATGACTGTCTCCTTGAAATAG
YOL3	CtaCGGCAGCCGCTGGATTGTTATTACTCGCG GCCCAGCCGGCCATGGCccag
YOL4	GTTCTGCTCCACTTCCTTCTGGGCCATGGCCG GCTGGGCCG
YOL5	CAGAAGGAAGTGGAGCAGAAC
YOL6	CTTCTTAAAGAATTCTTAATTAACCTAGGTTA TTAGGAACTTTCTGGGCTGGGGAAG
YOL7	GTTAATTAAGAATTCTTTAAGAAGGAGATATA CATATGAAAAAATTATTATTCGCAATTC
YOL8	CGCGCTGTGAGAATAGAAAGGAACAACTAAAG GAATTGCGAATAATAATTTTTTCATATG
YOL9	CTTTCTATTCTCACAGCGCGCAGGCTGGTGTC ACTCAGAC
YOL10	ATGATGTCTAGATGCGGCCGCGTCTGCTCTAC CCCAGGCCTC
YOL11	GCATCTAGACATCATCACCATCATCACTAGAC TGTTGAAAGTTGTTTAGCAAAAC
YOL12	CTAGAGGGTACCTTATTAAGACTCCTTATTAC GCAGTATG

Example 3 – Expression of fusions of bacterial coat protein and heterodimeric A6 TCR in E. coli.

In order to validate the construct made in Example 2, phage particles displaying the heterodimeric A6 TCR containing a non-native disulfide inter-chain bond were prepared using methods described previously for the generation of phage particles displaying antibody scFvs (Li *et al*, 2000, Journal of Immunological Methods **236:** 133-146) with the following modifications. *E. coli* XL-1-Blue cells containing pEX746:A6 phagemid (i.e. the phagemid encoding the soluble A6 TCR α chain and an A6 TCR β chain fused to the phage gIII protein produced as described in Example 2) were used to inoculate 5 ml of Lbatg (Lennox L broth containing 100μg/ml of ampicillin, 12.5 μg/ml tetracycline and 2% glucose), and then the culture was incubated with shaking at 37°C overnight (16 hours). 50 μl of the overnight culture was used to inoculate 5 ml of TYPatg (TYP is 16g/l of peptone, 16g/l of yeast extract, 5g/l of NaCl and 2.5g/l of K_2HPO_4), and then the culture was incubated with shaking at 37°C until OD_{600nm} = 0.8. Helper phage M13 K07 was added to the culture to the final concentration of 5 X 10^9 pfu/ml. The culture was then incubated at 37°C stationary for thirty minutes and then with shaking at 200 rpm for further 30 minutes. The medium of above culture was then changed to TYPak (TYP containing 100μg/ml of ampicillin, 25 μg/ml of kanamycin), the culture was then incubated at 25°C with shaking at 250 rpm for 36 to 48 hours. The culture was then centrifuged at 4°C for 30 minutes at 4000 rpm. The supernatant was filtrated through a 0.45 μm syringe filter and stored at 4°C for further concentration or analysis.

The fusion protein of filamentous coat protein and heterodimeric A6 TCR containing a non-native disulfide inter-chain bond was detected in the supernatant by western blotting. Approximately 10^{11} cfu phage particles were loaded on each lane of an SDS-PAGE gel in both reducing and non-reducing loading buffer. Separated proteins were primary-antibody probed with an anti-M13 gIII mAb, followed by a second antibody conjugated with Horseradish Peroxidase (HRP). The HRP activity was then detected with Opti-4CN substrate kit from Bio-Rad (Figure 5). Theses data indicated that

disulfide-bonded A6 TCR of clone 1 is fused with filamentous phage coat protein, gIII protein.

Example 4 – Detection of functional heterodimeric A6 TCR containing a non-native disulfide inter-chain bond on filamentous phage particles

The presence of functional (HLA-A2-tax binding) A6 TCR displayed on the phage particles was detected using a phage ELISA method.

TCR-Phage ELISA

Binding of the A6 TCR-displaying phage particles to immobilised peptide-MHC in ELISA is detected with primary rabbit anti-fd antisera (Sigma) followed by alkaline phosphatase (AP) conjugated anti-Rabbit mAb (Sigma). Non specific protein binding sites in the plates can be blocked with 2% MPBS or 3% BSA-PBS

Materials and reagents

1. Coating buffer, PBS
2. PBS: 138mM NaCl, 2.7mM KCl, 10mM Na_2HPO_4, 2mM KH_2PO_4
3. MPBS , 3% marvel-PBS
4. PBS-Tween: PBS, 0.1% Tween-20
5. Substrate solution, Sigma FAST pNPP, Cat# N2770

Method

1. Rinse NeutrAvidin coated wells twice with PBS.
2. Add 25µl of biotin-HLA-A2 Tax or biotin-HLA-A2 NYESO in PBS at concentration of 10 µg/ml, and incubate at room temperature for 30 to 60 min.
3. Rinse the wells twice with PBS
4. Add 300 µl of 3% Marvel-PBS, and incubate at room temperature for 1hr. Mix the TCR-phage suspension with 1 volume of 3% Marvel-PBS and incubate at room temperature.

5. Rinse the wells twice with PBS

6. Add 25 µl of the mixture of phage-A6 TCR/Marvel-PBS, incubate on ice for 1hr

7. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.

8. Add 25 µl of ice cold rabbit anti-fd antibody diluted 1:1000 in Marvel-PBS, and incubate on ice for 1hr

9. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.

10. Add 25 µl of ice cold anti-rabbit mAb-Ap conjugate diluted 1:50,000 in Marvel-PBS, and incubate on ice for 1hr

11. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.

12. Add 150 µl of Alkaline phosphatase yellow to each well and read the signal at 405nm

The results presented in Figure 6 indicate clone 1 produced a phage particle displaying an A6 TCR that can bind specifically to its cognate pMHC. (HLA-A2 Tax)

Analysis of the DNA sequence of this displayed A6 TCR revealed the presence of an 'opal' stop codon in the TCR β chain not present in the corresponding sequence of the expression vector construct of Example 2. This codon is 'read-through' with low frequency by ribosomes of the *E.coli* strain utilised resulting in the insertion of a tryptophan residue at this site and a much-reduced overall level of full-length β chain expression. From this observation it was inferred that only cells expressing this mutated A6 TCR sequence had survived the culture rounds of Example 3, and that

therefore the high levels of A6 TCR predicted to be expressed by the original expression vector were toxic to the host cells.

Example 5 – single- chain TCR (scTCR) ribosome display

Construction of Ribosome display scTCR vectors for use in generation of ribosome display PCR templates.

Ribosome display constructs were cloned into the readily available DNA plasmid pUC19 in order to generate an error free and stable DNA PCR template from which to conduct subsequent ribosome display experiments. Vector construction was undertaken in two steps so as to avoid the use of large oligonucleotide primers (with their associated error problems). The final A6 scTCR-C-Kappa DNA ribosome display construct is shown in a schematic form in figure 7a and both DNA and protein sequences are shown in Figure 7b. This construct can be excised from pUC19 as a Pst1/EcoR1 double digest.

The molecular cloning methods for constructing the vectors are described in "Molecular cloning:. A laboratory manual, by J. Sambrook and D. W. Russell". Primers listed in Table 2 are used for construction of the vectors. The PCR programme utilised was as follows – 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 30 seconds, 55°C for 20 seconds and 72°C for 120 seconds, followed by 1 cycles of 72°C for 5 minutes, and then hold at 4°C. The Pfu DNA polymerase is purchased from Strategene. Oligonucleotide primers used are described in table 2.

Construction of pUC19-T7- Step 1

The construction of pUC19-T7 is described below; the construction results in a pUC19 vector containing a T7 promoter region followed by a short space region and the an optimum eukaryotic Kozak sequence. This is an essential part of the ribosome display construct as it is required for the initiation of transcription of any attached sequence in rabbit reticulocyte lysates. Sequences for ribosome display such as the A6scTCR-

Ckappa can be ligated into the pUC19-T7 vector between the Nco1 and EcoR1 restriction sites.

Equimolar amounts of the primer Rev-link and For-link were annealed by heating to 94°C for 10 min and slowly cooling the reaction to room temperature. This results in the formation of a double stranded DNA complex that can be seen below.

```
5'AGCTGCAGCTAATACGACTCACTATAGGAACAGGCCACCATGG
      CGTCGATTATGCTGAGTGATATCCTTGTCCGGTGGTACCCTAG 3'
```

The 5' region contains an overhanging sticky end complimentary to a HindIII restriction site whilst the 3' end contains a sticky end that is complimentary to a BamH1 restriction site.

The annealed oligonucleotides were ligated into Hind III/BamHI double-digested pUC19 which had been purified by agarose gel electrophoresis, excised and further purified with the Qiagen gel extraction kit. The ligations were transformed into *E. coli* XL1-BLUE. Individual pUC19-T7 clones were sequenced to confirm the presence of the correct sequence. The sequence is shown in Figure 8.

Construction of A6scTCR-C-Kappa vector – Step 2.

Construction of the single chain A6scTCR-C-Kappa DNA sequence requires the generation of three PCR fragments that must then be assembled into one A6scTCR-C-Kappa fragment. The fragments consist of (a.) the A6 TCR alpha chain variable region flanked by a Nco1 site in the 5' region and a section of Glycine Serine linker in the 3' region flanked by a BamH1 restriction site. This product was generated via a standard PCR of the vector pEX202 with the primers 45 and 50 (See Table 2). Fragment (b.) A6 TCR beta variable and constant region flanked by a BamH1 restriction site in the 5' region followed by a section of Glycine Serine linker. This product was generated via a standard PCR of the vector pEX207 with the primers 72 and 73 (See Table 2).

Fragment (c.) Portion of a human C-kappa region generated by a standard PCR of the p147 vector with the primers 61-60 (See Table 2). All PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit.

Fragments (b.) and (c.) were fused by a standard overlap PCR via the complementarity in their primer sequences 73 and 61(See Table 2). The PCR was carried out via the primers 72 and 60 (See Table 2). The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit. This fragment is termed (d.).

Fragment (a.) was double digested with Nco1 and BamH1 whilst fragment (d.) was double digested with BamH1 and EcoR1. pUC19-T7 was double digested with Nco1 and EcoR1. All digested DNA products were run on a 1.2% TBE agarose gel and DNA bands of the correct size were excised and purified using the Qiagen gel extraction kit. The digested pUC19-T7, fragments (a.) and (d.) were ligated and transformed into E. coli XL1-BLUE. Transformants were sequenced to confirm the correct sequence. The sequence of the A6scTCR-C-Kappa ribosome display construct that was cloned into pUC19 is shown in Figure 9 flanked by its Pst1 and EcoR1 sites.

Table 2.

Oligonucleotides used (Purchased from MWG).

Rev-Link	5 ' GATCCCATGGTGGCCTGTTCCTATAGTGAGTCGTATTAGCTGC
For-Link	5 ' AGCTGCAGCTAATACGACTCACTATAGGAACAGGCCACCATGG
45-A6	5 ' CCACCATGGGCCAGAAGGAAGTGGAGCAGAACTC
7 A6-Beta(RT-PCR)(a)	5 ' CGAGAGCCCGTAGAACTGGACTTG
49-A6-BamH1-F	5 ' GTGGATCCGGCGGTGGCGGGTCGAACGCTGGTGTCA CTCAGACCCC
50-A6-BamH1-R	5 ' CCGGATCCACCTCCGCCTGAACCGCCTCCACCGGTGACCACAAC CTGGGTCCCTG
60-Kappa-rev-EcoR1	5' CTGAGAATTCTTATGACTCTCCGCGGTTGAAGCTC
61-Betac-Kappa-for1	5' TGACGAATTCTGACTCTCCGCGGTTGAAGCTC
71 T7-Primer	5' AGCTGCAGCTAATACGACTCACTATAGG
72 A6-beta	5' GGCCACCATGGGCAACGCTGGTGTCACTCAGACCCC
73-A6-cons-rev	5' TGAACCGCCTCCACCGTCTGCTCTACCCCAGGCCTCGGCG
75 Kappa-rev	5' TGACTCTCCGCGGTTGAAGCTC

Demonstration of the production of sc A6 TCR-C-Kappa by In vitro transcription translation.

Preparation of scA6 TCR-C-Kappa PCR product for In vitro transcription translation.

Here we describe the synthesis of sc A6 TCR-C-Kappa via *In vitro* transcription translation in the presence of biotinylated lysine and its subsequent detection by western blotting and detection with alkaline phosphatase labelled streptavidin.

The sc A6 TCR-C-Kappa PCR product was prepared in a standard PCR reaction using the vector sc A6 TCR-C-Kappa as template and PCR primers 71 and 60. Primer 60 contains a stop codon to allow the release of the scTCR from the ribosome. Pfu

polymerase (Strategene) was used for increased fidelity during PCR synthesis. The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit.

The transcription translation reactions were carried out using the Ambion PROTEINscript II Linked transcription translation kit Cat 1280-1287 with 300ng of the above described PCR product. Three transcription translation reactions were set up according to the manufactures protocol. The one modification was the addition of biotinylated lysine from the Transcend™ Non-Radioactive Translation Detection System.

Reaction 1 sc A6 TCR-C-Kappa 300ng with 2µl biotinylated lysine

Reaction 2 sc A6 TCR-C-Kappa 300ng without 2µl biotinylated lysine

Reaction 3 No DNA control with 2µl biotinylated lysine.

Two microliters of each reaction was run on a 4-20% Novex gradient SDS-PAGE gel (Invitrogen). Additionaly a number of dilutions of a control biotinylated TCR were also run. The gel was blotted and the proteins detected with streptavidin alkaline phosphatase and subsequently colometrically developed with Western Blue ® Stabilized Substrate for Alkaline Phosphatase as described in the Transcend™ Non-Radioactive Translation Detection System protocol. The western blot is shown in Figure 10.

In the no DNA control and A6scTCR-C-Kappa reaction without biotinylated lysine no band of approximately the correct size can be seen as expected whilst in the A6scTCR-C-Kappa reaction in the presence of biotinylated lysine a band of approximately the correct size can be seen. This demonstrates the synthesis of the sc A6 TCR-C-Kappa TCR by *In vitro* transcription translation.

Preparation of sc A6 TCR-C-Kappa ribosome display PCR product.

The sc A6 TCR-C-Kappa PCR product was prepared in a standard PCR reaction using the vector A6scTCR-C-Kappa as template and PCR primers 71 and 75 (See Table 2).

Primer 75 does not contain a stop codon. Pfu polymerase (Strategene) was used for increased fidelity during PCR synthesis. The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size were excised and purified using the Qiagen gel extraction kit.

Ribosome Display Process

Transcription and translation of sc A6 TCR-C-Kappa

The transcription / translation reactions were carried out using the Ambion PROTEINscript II Linked transcription translation kit (Cat No. 1280-1287)

Transcription reactions

The following transcription reactions were set up in Ambion 0.5 ml non stick tubes (Cat No. 12350).

Contents	tube 1 **(Normal A6)**	2 **(Control)**
Water	4.53 µl	5.7µl
Template (PCR product)	**Sc A6 TCR-C-Kappa PCR product 1.17µl (300 ng)**	No DNA
5X transcription mix	2 µl	2µl
Enzyme mix	2µl	2µl
Superasin Rnase inhibitor ambion	0.3µl	0.3µl
Final volume	10µl	10µl

The tubes were incubated at 30°C for 60 min on a PCR block with the hot lid off.

5 *Translation reactions*

The following translation reactions were set up in Ambion 0.5 ml non stick tubes.

Contents	1 (Normal A6)	2 (Control)
Reticulocyte Lysate	105µl	105 µl
25mM Mg-Acetate	3µl	3 µl
Translation Mix	7.5µl	7.5 µl
Methionine	7.5µl	7.5 µl
Water	18µl	18 µl
Superasin Rnase inhibitor	3µl	3 µl
Transcription reaction	6µl tube 1 above	6µl tube 2 above

10 Each tube contains enough for 3x50µl selections. The tubes were mixed and incubated at 30°C for 60 min on a PCR block with the hot lid off. After 30 min 3 Unit of RQ1 Rnase free Dnase (Promega) was added to destroy the original DNA template in tube 1 and 3 Unit RQ1 Rnase free Dnase (Promega) in tube 2. After 60 min 18µl of Heparin solution was added to translation reaction 2 and 18µl of Heparin solution was added to 15 translation reaction 1. Samples were stored on ice ready for selection against HLA-coated beads.

Coating of magnetic beads.

20µl of resuspended Streptavidin Magnetic Particles (Roche Cat. No. 1641778) were 20 transferred into a sterile Rnase free 1.5 ml eppendorf tube. The beads were immobilised with a Magnetic Particle Separator (Roche Cat. No. 1641794) and the supernatant was removed. The beads were then washed with 100 µl of Rnase free 1 X

PBS (10 x PBS Ambion Cat No. 9624, Ambion H_2O Cat No. 9930) the beads were immobilised and the supernatant was removed. A total of 3 PBS washes were carried out.

The beads were resuspended in 20µl of PBS and the contents split evenly between two tubes (10µl each). One tube will be used to produce control-blocked beads and the other tubes to produce HLA-A2-Tax coated beads.

To the control beads tube 80µl of BSA/Biotin solution was added and mixed. The BSA/Biotin solution was made up as follows. 10µl of a 0.2M Tris base 0.1M Biotin solution was added to 990µl of PBS 0.1 % BSA (Ambion Ultrapure Cat No. 2616). Also 20 µl of Heparin solution (138 mg/ml Heparin (Sigma H-3393) in 1 x PBS) was added and the solution mixed. The beads were incubated at room temperature for 1 hour with intermittent mixing. The beads were then washed three times with 100µl of PBS and were resuspended in 10 µl of PBS, 0.1% BSA.

The HLA-TAX coated beads were prepared as follows. 40 µl of HLA-A2-Tax(1.15 mg/ml prepared as described in WO99/60120) was added to the 10 µl of beads and mixed. The beads were incubated at room temperature for 15 min and then 20 µl of BSA 50mg/ml Ambion Cat 2616 and 20 µl of heparin solution (see above) were added and mixed. The beads were incubated for a further 45 min and then 20 µl of BSA/Biotin solution was added. The beads were then washed three times with 100 µl of PBS and were re-suspended in 10 µl of PBS, 0.1% BSA.

Panning with magnetic beads

The sc A6 TCR translation reaction was split into three 50µl aliquots and each aliquot received either 2µl of the following beads:

Control (no HLA)

HLA-A2-Tax

HLA-A2-Tax plus 10µg soluble scA6 TCR

A control translation reaction was also carried out and split into three 50µl aliquots and each aliquot received either 2µl of the following beads

Control (no HLA)

HLA-A2-Tax

HLA-A2-Tax plus 10µg soluble sc A6 TCR

This gave a total of six tubes. The tubes were incubated on a PCR block at 5°C for 60 min with intermittent mixing.

The beads were then washed three times with 100µl ice cold buffer (PBS, 5mM Mg-acetate, 0.2% Tween 20(Sigma Rnase free). Each aliquot of beads were then re-suspended in 50µl of 1 x RQ1 Dnase digestion buffer containing 1µl (40 U) of Superasin and 1µl (1U) of RQ1 Dnase. The beads were incubated on a PCR block for 30 min at 30°C.

The beads were then washed three times with 100µl ice cold buffer (PBS, 5mM Mg-acetate, 0.2% Tween 20) and once with ice cold H_2O. The beads were re-suspended in 10µl of Rnase free H_2O. The beads were then frozen ready for RT-PCR.

RT-PCR of sc A6 TCR-C-Kappa mRNA on beads rescued from the ribosome display reactions.

The RT PCR reactions on the beads were carried out using the Titan one tube RT-PCR kit cat 1855476 as described in the manufacturers protocols. Two microliters of beads were added into each RT-PCR reaction along with the primers 45 and 7 and 0.3µl of Superasin Rnase inhibitor.

For each RT-PCR reaction a second PCR only reaction was set up which differed only by the fact that no reverse transcriptase was present just Roche high fidelity polymerase. This second reaction served as a control for DNA contamination.

Additionally a RT-PCR positive control control was set up using 1ng of the vector sc A6 TCR-C-Kappa.

The reactions were cycled as follows. An RT-PCR step was carried out by incubation of the samples at 50°C for 30 min followed by the inactivation of the reverse transcriptase by incubation at 94°C for 3 min on a PCR block.
The reactions were PCR cycles as follows for a total of 38 cycles:

94°C 30 seconds
55°C 20 seconds
68°C 130 seconds.
The PCR reaction was finished by incubation at 72°C for 4 minutes.

Great care was taken during all ribosome display steps to avoid Rnase contamination. The RT-PCR and PCR reactions were run on a 1.6% TBE agarose gel which can be seen in Figure 11. Analysis of the gel shows that there is no DNA contamination and that all PCR products are derived from mRNA. The DNA band of the correct size in lane 2 demonstrates that ribosome displayed sc A6 TCR-C-Kappa was selected out by HLA-A2-Tax coated beads. Lane 3 shows that we can inhibit this specific selection of ribosome-displayed sc A6 TCR-C-Kappa by the addition of soluble sc A6 TCR. The significant reduction in the band intensity in lane 3 relative to the uninhibited sample in lane 2 demonstrates this. No binding of ribosome-displayed sc A6 TCR-C-Kappa could be shown against control non-HLA coated beads.

Example 6 – Sequence Analysis of A6 TCR clones displayed on phage particles and methods to improve display characteristics

After the construction of vectors for displaying A6 TCR on phage by PCR and molecular cloning, bacterial clones that can produce phage particles displaying A6 TCR were screened by phage ELISA as described in Example 4. Three different clones were identified that gave specific binding to HLA-A2-tax in the ELISA binding

assay. These clones all contained mutations in the 'wild-type' A6 TCR DNA or in the associated regulatory sequences, which are described in the following table:

Functional clones from screening TCR A6 displayed on phage

Name	Feature	
Clone 7	The third ribosome-binding site, which is located in front of vβ gene, is mutated from AAGGAGA to AAGGGGA.	
Clone 9	An opal codon is introduced in vβ CDR3.	Full DNA and amino acid sequence in Figures 12a & 12b
Clone 49	An amber codon is introduced in vβ FR1. This mutation introduces a 'silent' mutation that does not affect the resulting amino acid sequence	Full DNA sequence in Figures 13a

These clones all contained mutations that are likely to cause a reduction in the expression levels of the A6 TCR β chain. It was inferred that low expression clones were selected over high expression clones as a result of cell toxicity caused by high expression levels of TCR.

Example 7– Mutagenesis of A6 TCR CDR3 regions

The CDR3 regions of the A6 TCR were targeted for the introduction of mutations to investigate the possibility of generating high affinity mutants.

Overlapping PCR was used to modify the sequence of α and β CDR3 regions to introduce two unique restriction sites *Hind III* for α chain, with oligos of YOL54, 5'CAGCTGGGGGAAGCTTCAGTTTGGAGCAG3' and YOL55, 5'CTGCTCCAAACTGAAGCTTCCCCCAGCTG3', and *Xho* I for β chain, with

oligos of YOL56 5'GTACTTCTGTGCCTCGAGGCCGGGACTAG3' and YOL57 5'CTAGTCCCGGCCTCGAGGCACAGAAGTAC3'.

PCR was used to introduce mutations for affinity maturation. The A6 TCR clone 9 (incorporating an introduced opal codon in the β chain CDR3 sequence) was used as a source of template DNA, and TCR chains were amplified with the mutation primers (detailed in the following table) and YOL22 5'CATTTTCAGGGATAGCAAGC3' (β-chains) or YOL13 5'TCACACAGGAAACAGCTATG3' (α-chains).

Primers for introducing mutation at CDR3 of A6 β chain and α chain

Primer name	Sequence 5' to 3'
YOL59	TGTGCCTCGAGGNNKNNKNNKNNKNNKN NKCGACCAGAGCAGTACTTCG
YOL60	TGTGCCTCGAGGCCGNNKNNKNNKNNKN NKNNKCCAGAGCAGTACTTCGGGC
YOL61	TGTGCCTCGAGGCCGNNKNNKNNKNNKN NKNNKCGACCAGAGCAGTACTTCG
YOL62	TGTGCCTCGAGGCCGNNKNNKNNKNNKN NKNNKGGAGGGCGACCAGAGCAG
YOL63	TGTGCCTCGAGGCCGGGANNKNNKNNKN NKNNKNNKGGGCGACCAGAGCAGTAC
YOL68	TGTGCCTCGAGGNNKNNKNNKNNKNNKN NKCCAGAGCAGTACTTCGggc
YOL69	TGTGCCTCGAGGNNKNNKNNKNNKNNKN NKGAGCAGTACTTCGggccg
YOL70	TGTGCCTCGAGGNNKNNKNNKNNKNNKN NKCAGTACTTCGggccgggc
YOL71	TGTGCCTCGAGGccgNNKNNKNNKNNKg ggCGACCAGAGCAGTACTTCG
YOL58	AAACTGAAGCTTMNNMNNMNNMNNMNNT GTAACGGCACAGAGGTAG
YOL72	AAACTGAAGCTTMNNMNNgctgtcMNNT GTAACGGCACAGAGGTAG
YOL73	AAACTGAAGCTTMNNMNNMNNgctgtcM NNTGTAACGGCACAGAGGTAG
YOL74	AAACTGAAGCTTMNNMNNgctgtcMNNA ACGGCACAGAGGTAG

α-chain fragments were digested with *Nco I* and *HindIII* and re-purified using a Qiagen kit and vector was prepared by digesting clone 9 with *Nco I* and *HindIII* followed by gel purification using a Qiagen kit. β-chain fragments were digested with

Xho I and *Not I* and re-purified using a Qiagen kit and vector was prepared by digesting clone 9 with *Xho I* and *Not I* followed by gel purification using a Qiagen kit. Purified inserts and vectors at 3:1 molar ratio were mixed with T4 ligase buffer, T4 ligase and nuclease-free water. The ligations were carried out at 16°C water bath overnight. For each mutation-library, a total of 0.5 to 1μg purified ligated products were electroporated into *E. coli* TG1 at ratio of 0.2μg DNA per 40 μl of electroporation-competent cells (Stratagen) following the protocols provided by the manufacturer. After electroporation, the cells were re-suspended immediately with 960μl of SOC medium at 37°C and plated on a 244mm x244mm tissue culture plate containing YTE (15g Bacto-Agar, 8g NaCl, 10g Tryptone, 5g Yeast Extract in 1 litre) supplemented with 100μg/ml ampicillin and 2% glucose. The plate was incubated at 30°C over night. The cells were then scraped from the plates with 5 ml of DYT (16g Trytone, 10g Yeast extract and 5g NaCl in 1 litre, autoclaved at 125°C for 15 minutes) supplemented with 15% glycerol.

In order to make phage particles displaying the A6 TCR, 500 ml of DYTag (DYT containing 100 μg/ml of ampicillin and 2% glucose) was inoculated with 500 to 1000 μl of the library stocks. The culture was grown until OD(600nm) reached 0.5. 100 ml of the culture was infected with helper phage (M13 K07 (Invitrogen), or HYPER PHAGE (Progen Biotechnik, GmbH 69123 Heidelberg), and incubated at 37°C water bath for 30 minutes. The medium was replaced with 100 ml of DYTak (DYT containing 100 μg/ml ampicillin and 25 μg/ml of kanamycin). The culture was then incubated with shaking at 300 rpm and 25°C for 20 to 36 hours.

Example 8 – Isolation of high affinity A6 TCR mutants

The isolation of high affinity A6 TCR mutants was carried out using two different methods.

The first method involves selecting phage particles displaying mutant A6 TCRs capable of binding to HLA-A2 Tax complex using Maxisorp immuno-tubes

(Invitrogen) The immuno-tubes were coated with 1 to 2 ml 10μg/ml streptavidin in PBS overnight at room temperature. The tubes were washed twice with PBS, and then 1 ml of biotinylated HLA-A2 Tax complex at 5μg/ml in PBS was added and incubated at room temperature for 30 minutes. The rest of the protocol for selection of high affinity binders is as described previously (Li *et al.* (2000) *Journal of Immunological Methods* 236: 133-146), except for the following modifications. The selection was performed over three or four rounds. The concentrations of biotinylated HLA-A2 Tax complex were 5μg/ml for the first round of selection, 0.5 μg/ml for the second, 0.05 μg/ml for the third and 0.005 μg/ml for the fourth round of selection. M13 K07 helper phage were used in rounds one and two, and hyper phage were used in subsequent rounds, for the selection.

The second method utilised was the selection of phage particles displaying mutant A6 TCRs capable of binding to HLA-A2 Tax complex in solution. Streptavidin-coated paramagnetic beads (Dynal M280) were pre-washed according to manufacturer's protocols. Phage particles, displaying mutated A6 TCR at a concentration of 10^{12} to 10^{13} cfu, were pre-mixed with biotinylated HLA-A2 Tax complex at concentrations of $2x10^{-8}$M, $2x10^{-9}$M, $2x10^{-10}$M and $2x\ 10^{-11}$M for first, second, third and fourth-round of selections respectively. The mixture of A6 TCR-displaying phage particles and HLA-A2 Tax complex was incubated for one hour at room temperature with gentle rotation, and A6 TCR-displaying phage particles bound to biotinylated HLA-A2 Tax complex were captured using 200 μl (round 1) or 50μl (round 2, 3, and 4) of streptavidin-coated M280 magnetic beads. After capture of the phage particles, the beads were washed a total of ten times (three times in PBStween20, twice in PBStween 20 containing 2% skimmed milk powder, twice in PBS, once in PBS containing 2% skimmed milk powder, and twice in PBS) using a Dynal magnetic particle concentrator. After final wash, the beads was re-suspended in 1ml of freshly prepared 100mM triethylamine pH11.5, and incubated for 5 to 10 minutes at room temperature with gentle rotation. Phage particles eluted from the beads were neutralized immediately with 300 μl of 1M tris-HCl pH7.0. Half of the eluate was used to infect 10 ml of *E.coli* TG1 at OD(600nm)=0.5 freshly prepared for the amplification of the selected phage particles

according to the methods previously described (Li *et al.*, (2000) *Journal of Immunological Methods* 236: 133-146).

After the third or fourth round of selection, 95 colonies were picked from the plates and used to inoculate 100 µl of DYTag in a 96-well microtiter plate. The culture was incubated at 37°C with shaking overnight. 100 µl of DYTag was then sub-inoculated with 2 to 5 µl of the overnight cultures, and incubated at 37°C with shaking for 2 to 3 hours or until the culture became cloudy. To infect the cells with helper phage, the culture was infected with 25 µl of DYTag containing 5 x 10^9 pfu helper phages, and incubated at 37°C for 30 minutes. The medium was replaced with DYTak. The plates were incubated at 25°C for 20 to 36 hours with shaking at 300 rpm. The cells were precipitated by centrifugation at 3000g for 10 minutes at 4°C. Supernatants were used to screen for high affinity A6 TCR mutants by competitive phage ELISA as follows.

Nunc-Immuno Maxisorp wells coated with streptavidin were rinsed twice with PBS. 25 µl 5 µg/ml biotinylated HLA-A2-Tax complex was added to each well and these were incubated at room temperature for 30 to 60 minutes, and followed by two PBS rinses. Non-specific protein binding sites in the wells were blocked by the addition of 300 µl 3% skimmed milk in PBS followed by incubation at room temperature for 2 hours. In order to prepare phage particles displaying the heterodimric A6 TCR, phage particles were mixed with 3% skimmed milk in PBS containing 0, 20, and 200 nM HLA-A2-Tax, followed by incubated at room temperature for 1 hour. The phage is added to the wells coated with HLA-A2-Tax and incubated at room temperature for 1 hour, followed by 3 washes with PBS containing 0.1% tween 20 and then 3 washes with PBS. The bound TCR-dispalying phage particles are detected with an anti-fd antibody (Sigma) as described in Example 4.

Several high affinity A6 TCR mutants were identified, and the CDR3 sequences are listed in the two following tables along with the corresponsding wild-type sequences. ~~Amber stop codons (*) were found in all β-chain mutants and one α-chain mutant.~~

A6 TCR β chain mutants

clone	CDR3 sequence
Wild Type	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCAGAGCAGTAG A S R P G L A G G R P E Q Y
134	GCCTCGAGGCCGGGGCTGATGAGTGCGTAGCCAGAGCAGTAC A S R P G L **M S A** * P E Q Y
86	GCCTCGAGGCCGGGGCTGAGGTCGGCGTAGCCAGAGCAGTAC A S R P G L **R S A** * P E Q Y
87	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCAGAGGCGTAG A S R P G L A G G R P E **A** *
89	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCAGAGGATTAG A S R P G L A G G R P E **D** *
85	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCAGATCAGTAG A S R P G L A G G R P **D** Q *
83	GCCTCGAGGCCGGGTCTGTAGGCTGGGCGACCAGAGCAGTAC A S R P G L * **A G** R P **E** Q Y
1	GCCTCGAGGCCGGGGCTGGTTCCGGGGCGACCAGAGCAGTAG A S R P G L **V P** G R P E Q *
2	GCCTCGAGGCCGGGGCTTGTGTCTGCTTAGCCAGAGCAGTAC A S R P G L **V S A** * P E Q Y
111	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCACATCCGTAG A S R P G L A G G R P **H P** *
125	GCCTCGAGGCCGGGACTAGCGGGAGGGCGACCAGATGCGTAG A S R P G L A G G R P **D A** *
133	GCCTCGAGGCCGGGTCTGATTAGTGCTTAGCCAGAGCAGTAC A S R P G L **I S A** * P E Q Y

A6 TCR α chain mutants

Clone	CDR3
Wild Type	GCCGTTACAACTGACAGCTGGGGGAAGCTTCAG A V T T D S W G K L Q
149	GCCGTTACAACTGACAGCTGGGGGCCGCTTCAG A V T T D S W G **P** L Q
65	GCCGTTACAACTGACAGCTGGGGGAAGATGCAG A V T T D S W G K **M** Q
66	GCCGTTACAACTGACAGCTGGGGGAAGTTGCAT A V T T D S W G K L **H**
153	GCCGTTACAACTGACAGCTGGGGGTAGCTTCAT A V T T D S W G * L **H**
71	GCCGTTACAACTGACAGCTGGGGGGAGCTTCAT A V T T D S W G **E** L **H**
70	GCCGTTACAACTGACAGCTGGGGGAGGCTGCAT A V T T D S W G **R** L **H**
121	GCCGTTACAACTGACAGCTGGGGGCAGCTTCAT A V T T D S W G **Q** L **H**

117	GCCGTTACAACTGACAGCTGGGGGAAGGTTCAT A V T T D S W G K **V** **H**
72	GCCGTTACAACTGACAGCTGGGGGAAGGTGAAT A V T T D S W G K **V** **N**
150	GCCGTTACAACTGACAGCTGGGGGAAGCTTCTG A V T T D S W G K L **L**

Example 9 – Production of soluble heterodimeric A6 TCR with non-native disulfide bond between constant regions, containing CDR3 mutations

Phagemid DNA encoding the high affinity A6 TCR mutants identified in Example 8 was isolated from the relevant *E.coli* cells using a Mini-Prep kit (Quiagen, UK)

PCR amplification using the phagemid DNA as a target and the following primers was used to amplify the soluble TCR α and β chain DNA sequences.

A6 TCR alpha chain forward primer
ggaattc atcgatg cagaaggaagtggagcag
ClaI restriction site is underlined)

Universal TCR alpha chain reverse primer
gtacacggccgggtcagggttctggatatac
(EagI restriction site is underlined)

A6 beta chain forward primer
tctctcattaatgaatgctggtgtcactcagacccc
(AseI restriction site is underlined)

Universal beta chain reverse primer
tagaaaccggtggccaggcacaccagtgtggc
(AgeI restriction site is underlined)

In the case of the TCR β chain a further PCR stitching was carried out to replace the amber stop codon in the CDR3 region with a codon encoding glutamic acid. When an amber stop codon is suppressed in *E.coli*, a glutamine residue is normally introduced

instead of the translation being stopped. Therefore, when the amber codon-containing TCR is displayed on the surface of phage, it contains a glutamine residue in this position. However, when the TCR β –chain gene was transferred into the expression plasmid, a glutamic acid residue was used as an alternative to glutamine. The primers used for this PCR stitching were as follows.

YOL124 CTGCTCTGGTTCCGCACTC
YOL125 GAGTGCGGAACCAGAGCAG

The DNA sequence of the mutated soluble A6 TCR β chain was verified by automated sequencing (see Figure 14a for the mutated A6 TCR β chain DNA sequence and 14b for the amino acid sequence encoded thereby). Figure 14c shows the mutated A6 TCR β chain amino acid sequence without the glutamine to glutamic acid substitution, i.e. the sequence that was present in Clone 134 as isolated by phage-ELISA.

Theses A6 TCR α and β DNA sequences were then used to produce a soluble A6 TCR as described in WO 03/020763. Briefly, the two chains are expressed as inclusion bodies in separate *E.coli* cultures. The inclusion bodies are then isolated, de-natured and re-folded together *in vitro*.

Example 10 – BIAcore surface plasmon resonance characterisation of a high affinity A6 TCR binding to HLA-A2 Tax.

A surface plasmon resonance biosensor (BIAcore 3000™) was used to analyse the binding of the high affinity clone 134 A6 TCR (See Figures 15a & 15b for the full DNA and amino acid sequences of the mutated TCR β chain respectively) to the HLA-A2 Tax ligand. This was facilitated by producing pMHC complexes (described below) which were immobilised to a streptavidin-coated binding surface in a semi-oriented fashion, allowing efficient testing of the binding of a soluble T-cell receptor to up to four different pMHC (immobilised on separate flow cells) simultaneously. Manual injection of HLA complex allows the precise level of immobilised class I molecules to be manipulated easily.

Biotinylated class I HLA-A2 tax complexes were refolded *in vitro* from bacterially-expressed inclusion bodies containing the constituent subunit proteins and synthetic peptide, followed by purification and *in vitro* enzymatic biotinylation (O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). HLA-heavy chain was expressed with a C-terminal biotinylation tag which replaces the transmembrane and cytoplasmic domains of the protein in an appropriate construct. Inclusion body expression levels of ~75 mg/litre bacterial culture were obtained. The HLA light-chain or β2-microglobulin was also expressed as inclusion bodies in *E.coli* from an appropriate construct, at a level of ~500 mg/litre bacterial culture.

E. coli cells were lysed and inclusion bodies were purified to approximately 80% purity. Protein from inclusion bodies was denatured in 6 M guanidine-HCl, 50 mM Tris pH 8.1, 100 mM NaCl, 10 mM DTT, 10 mM EDTA, and was refolded at a concentration of 30 mg/litre heavy chain, 30 mg/litre β2m into 0.4 M L-Arginine-HCl, 100 mM Tris pH 8.1, 3.7 mM cystamine, mM cysteamine, 4 mg/ml peptide (e.g. tax 11-19), by addition of a single pulse of denatured protein into refold buffer at < 5°C. Refolding was allowed to reach completion at 4°C for at least 1 hour.

Buffer was exchanged by dialysis in 10 volumes of 10 mM Tris pH 8.1. Two changes of buffer were necessary to reduce the ionic strength of the solution sufficiently. The protein solution was then filtered through a 1.5μm cellulose acetate filter and loaded onto a POROS 50HQ anion exchange column (8 ml bed volume). Protein was eluted with a linear 0-500 mM NaCl gradient. HLA-A2-peptide complex eluted at approximately 250 mM NaCl, and peak fractions were collected, a cocktail of protease inhibitors (Calbiochem) was added and the fractions were chilled on ice.

Biotinylation tagged HLA-A2 complexes were buffer exchanged into 10 mM Tris pH 8.1, 5 mM NaCl using a Pharmacia fast desalting column equilibrated in the same buffer. Immediately upon elution, the protein-containing fractions were chilled on ice and protease inhibitor cocktail (Calbiochem) was added. Biotinylation reagents were then added: 1 mM biotin, 5 mM ATP (buffered to pH 8), 7.5 mM MgCl2, and 5 μg/ml

BirA enzyme (purified according to O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). The mixture was then allowed to incubate at room temperature overnight.

Biotinylated HLA-A2 complexes were purified using gel filtration chromatography. A Pharmacia Superdex 75 HR 10/30 column was pre-equilibrated with filtered PBS and 1 ml of the biotinylation reaction mixture was loaded and the column was developed with PBS at 0.5 ml/min. Biotinylated HLA-A2 complexes eluted as a single peak at approximately 15 ml. Fractions containing protein were pooled, chilled on ice, and protease inhibitor cocktail was added. Protein concentration was determined using a Coomassie-binding assay (PerBio) and aliquots of biotinylated HLA-A2 complexes were stored frozen at –20°C. Streptavidin was immobilised by standard amine coupling methods.

The interactions between the high affinity A6 Tax TCR containing a novel inter-chain bond and the HLA-A2 Tax complex or an irrelevant HLA-A2 NY-ESO combination, the production of which is described above, were analysed on a BIAcore 3000™ surface plasmon resonance (SPR) biosensor. SPR measures changes in refractive index expressed in response units (RU) near a sensor surface within a small flow cell, a principle that can be used to detect receptor ligand interactions and to analyse their affinity and kinetic parameters. The probe flow cells were prepared by immobilising the individual HLA-A2 peptide complexes in separate flow cells via binding between the biotin cross linked onto β2m and streptavidin which have been chemically cross linked to the activated surface of the flow cells. The assay was then performed by passing sTCR over the surfaces of the different flow cells at a constant flow rate, measuring the SPR response in doing so. Initially, the specificity of the interaction was verified by passing soluble A6 TCR at a constant flow rate of 5 µl min-1 over four different surfaces; one coated with ~1000 RU of HLA-A2 Tax complex, the second coated with ~1000 RU of HLA-A2 NY-ESO complex, and two blank flow cells coated only with streptavidin (see Figure 15).

The increased affinity of the mutated soluble A6 TCR made calculation of the kd for the interaction of this moiety with the HLA-A2 Tax complex difficult. However, the half-life ($t_{½}$) for the interaction was calculated to be 51.6 minutes (see Figure 16), which compares to a $t_{½}$ for the wild-type interaction of 7.2 seconds.

Example 11 – Production of vector encoding a soluble NY-ESO TCR containing a novel disulphide bond.

The β chain of the soluble A6 TCR prepared in Example 1 contains in the native sequence a BglII restriction site (AAGCTT) suitable for use as a ligation site.

PCR mutagenesis was carried as detailed below to introduce a BamH1 restriction site (GGATCC) into the α chain of soluble A6 TCR, 5' of the novel cysteine codon. The sequence described in Figure 2a was used as a template for this mutagenesis. The following primers were used:

```
                    |BamHI |
5'-ATATCCAGAACCCgGAtCCTGCCGTGTA-3'
5'-TACACGGCAGGAaTCcGGGTTCTGGATAT-3'
```

100 ng of plasmid was mixed with 5 µl 10 mM dNTP, 25 µl 10xPfu-buffer (Stratagene), 10 units Pfu polymerase (Stratagene) and the final volume was adjusted to 240 µl with H_2O. 48 µl of this mix was supplemented with primers diluted to give a final concentration of 0.2 µM in 50 µl final reaction volume. After an initial denaturation step of 30 seconds at 95°C, the reaction mixture was subjected to 15 rounds of denaturation (95°C, 30 sec.), annealing (55°C, 60 sec.), and elongation (73°C, 8 min.) in a Hybaid PCR express PCR machine. The product was then digested for 5 hours at 37°C with 10 units of DpnI restriction enzyme (New England Biolabs). 10 µl of the digested reaction was transformed into competent XL1-Blue bacteria and grown for 18 hours at 37°C. A single colony was picked and grown over night in 5 ml TYP + ampicillin (16 g/l Bacto-Tryptone, 16 g/l Yeast Extract, 5 g/l NaCl, 2.5 g/l

K_2HPO_4, 100 mg/l Ampicillin). Plasmid DNA was purified on a Qiagen mini-prep column according to the manufacturer's instructions and the sequence was verified by automated sequencing at the sequencing facility of Department of Biochemistry, Oxford University.

CDNA encoding NY-ESO TCR was isolated from T cells according to known techniques. CDNA encoding NY-ESO TCR was produced by treatment of the mRNA with reverse transcriptase.

In order to produce a vector encoding a soluble NY-ESO TCR incorporating a novel disulphide bond, A6 TCR plasmids containing the α chain BamHI and β chain BglII restriction sites were used as templates. The following primers were used:

```
                | NdeI |
5'-GGAGATATACATATGCAGGAGGTGACACAG-3'
5'-TACACGGCAGGATCCGGGTTCTGGATATT-3'
                | BamHI|


                |NdeI |
5'-GGAGATATACATATGGGTGTCACTCAGACC-3'
5'-CCCAAGCTTAGTCTGCTCTACCCCAGGCCTCGGC -3'
       |BglII|
```

NY-ESO TCR α and β-chain constructs were obtained by PCR cloning as follows. PCR reactions were performed using the primers as shown above, and templates containing the native NY-ESO TCR chains. The PCR products were restriction digested with the relevant restriction enzymes, and cloned into pGMT7 to obtain expression plasmids. The sequence of the plasmid inserts were confirmed by automated DNA sequencing. Figures 17a and 17b show the DNA sequence of the mutated NY-ESO TCR α and β chains respectively, and Figures 18a and 18b show the resulting amino acid sequences.

Example 12 - Construction of phage display vectors and cloning of DNA encoding NY-ESO TCR α and β chains into the phagemid vectors.

DNA encoding soluble NY-ESO TCR α and β chains incorporating novel cysteine codons to facilitate the formation of a non-native disulfide inter-chain bond, produced as described in Example 11 were incorporated into the phagemid vector pEX746 as follows.

The DNA encoding the two NY-ESO TCR chains were individually subjected to PCR in order to introduce cloning sites compatible with the pEX746 phagemid vector (containing DNA encoding A6 TCR clone 7) using the following primers:

For the NY-ESO TCR alpha chain

TRAV21

GCCGGCCATGGCCAAACAGGAGGTGACGCAGATTCCT

YOL6

CTTCTTAAAGAATTCTTAATTAACCTAGGTTATTAGGAACTTTCTGGGCTG GGGAAG

For the NY-ESO TCR beta chain

TRBV6-1/2/3/5/6/7/8/9

TCACAGCGCGCAGGCTGGTGTCACTCAGACCCCAAA

RT1

CGAGAGCCCGTAGAACTGGACTTG

The molecular cloning methods for constructing the vectors are described in "Molecular cloning: A laboratory manual, by J. Sambrook and D. W. Russell". Primers listed in table-1 are used for construction of the vectors. A example of the PCR programme is 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 5 seconds, 53°C for 5 seconds and 72°C for 90 seconds, followed by 1 cycles of 72°C for 10 minutes, and then hold at 4°C. The Expand hifidelity Taq DNA polymerase is purchased from Roche.

DNA encoding the clone 7 A6 TCR β chain was removed from pEX746 by digestion with restrictions enzymes BssHII and BglII. The correspondingly digested PCR DNA encoding the NY-ESO β chain was then substituted into the phagemid by ligation. The sequence of the cloning product was verified by automated sequencing.

Similarly, DNA encoding the clone 7 A6 TCR α chain was removed from pEX746 by digestion with restrictions enzymes NcoI and AvrII. The correspondingly digested PCR DNA encoding the NY-ESO α chain was then substituted into the phagemid already containing DNA encoding the NY-ESO TCR β chain by ligation. The sequence of the cloning product was verified by automated sequencing.

Figure 19 details the DNA and amino acid sequence of the NY-ESO TCR α and β chain as well as surrounding relevant sequence incorporated in the phagemid (pEX746:NY-ESO) respectively. The sequence preceeding the NcoI site (Figure 19) is the same as pEX746.

Example 13 – Expression of fusions of bacterial coat protein and heterodimeric NY-ESO TCR in E. coli.

Phage particles displaying the heterodimeric NY-ESO TCR containing a non-native disulfide inter-chain bond were prepared using methods described previously for the generation of phage particles displaying antibody scFvs (Li *et al*, 2000, Journal of Immunological Methods **236:** 133-146) with the following modifications. *E. coli* TG 1 cells containing pEX746:NY-ESO phagemid (i.e. the phagemid encoding the soluble NY-ESO TCR α chain and an NY-ESO TCR β chain fused to the phage gIII protein produced as described in Example 12) were used to inoculate 10 ml of 2x TY (containing 100μg/ml of ampicillin and 2% glucose), and then the culture was incubated with shaking at 37°C overnight (16 hours). 50 μl of the overnight culture was used to inoculate 10 ml of 2x TY (containing 100μg/ml of ampicillin and 2% glucose), and then the culture was incubated with shaking at 37°C until OD_{600nm} = 0.8. HYPERPHAGE Helper phage was added to the culture to the final concentration of 5 X 10^9 pfu/ml. The culture was then incubated at 37°C stationary for thirty minutes and then with shaking at 200 rpm for further 30 minutes. The medium of above culture

was then made up to 50 ml with 2x TY (containing 100μg/ml of ampicillin and 25 μg/ml of kanamycin), the culture was then incubated at 25°C with shaking at 250 rpm for 36 to 48 hours. The culture was then centrifuged at 4°C for 30 minutes at 4000 rpm. The supernatant was filtrated through a 0.45 μm syringe filter and stored at 4°C for further concentration. The supernatant was then concentrated by PEG precipitation and re-suspended in PBS at 10% of the original stored volume.

Example 14 – Detection of functional heterodimeric NY-ESO TCR containing a non-native disulfide inter-chain bond on filamentous phage particles

The presence of functional (HLA-A2-NY-ESO binding) NY-ESO TCR displayed on the phage particles in the concentrated suspension prepared in Example 13 was detected using the phage ELISA methods described in Example 4. Figure 20 shows the specific binding of phage particles displaying the NY-ESO TCR to HLA-A2-NY-ESO in a phage ELISA assay.

Example 15 - Construction of plasmids for cellular expression of HLA-DRA genes.

DNA sequences encoding the extracellular portion of HLA-DRA chains are amplified from cDNA isolated from the blood of a healthy human subject, using the polymerase chain reaction (PCR), with synthetic DNA primer pairs that are designed to include a Bgl II restriction site.

PCR mutagenesis is then used to add DNA encoding the Fos leucine zipper to the 3' end of the amplified sequencence.

DNA manipulations and cloning described above are carried out as described in Sambrook, J *et al*, (1989). Molecular Cloning - A Laboratory Manual. Second Edition. Cold Spring Harbor Laboratory Press, USA.

Figure 21 provides the DNA sequence of the HLA-DR β chain ready for insertion into the bi-cistronic expression vector. This figure indicates the position of the codons encoding the Fos leucine zipper peptide and the biotinylation tag.

Amino acid numbering is based on the mouse sequence (Kabat, 1991, Sequences of Proteins of Immunological Interest, 5th edition, US Dept of Health & Human Services, Public Health Service, NIH, Bethesda, MD 1-1137)

This DNA sequence is then inserted into a bi-cistronic baculovirus vector pAcAB3 (See Figure 22 for the sequence of this vector) along with DNA encoding the corresponding Class II HLA β chain for expression in Sf9 insect cells. This vector can be used to express any Class II HLA-peptide complex in insect cells.

Example 16. Construction of plasmids for cellular expression of HLA-DRB wild type and mutant genes.

DNA sequences encoding the extracellular portion of HLA-DRB chains are amplified from cDNA isolated from the blood of a healthy human subject, using the polymerase chain reaction (PCR), with synthetic DNA primer pairs that are designed to include a BamH1 restriction site.

PCR mutagenesis is then used to add DNA encoding the Jun leucine zipper to the 3' end of the amplified sequence and DNA encoding the Flu HA peptide loaded by the HLA-DR1 molecule to the 5' end of the sequence.

DNA manipulations and cloning described above are carried out as described in Sambrook, J *et al*, (1989). Molecular Cloning - A Laboratory Manual. Second Edition. Cold Spring Harbor Laboratory Press, USA.

Figure 23 provides the DNA sequence of the HLA-DR β chain ready for insertion into the bi-cistronic expression vector. This figure indicates the position of the codons encoding the Jun leucine zipper peptide and the Flu HA peptide.

Amino acid numbering is based on the mouse sequence (Kabat, 1991, Sequences of Proteins of Immunological Interest, 5th edition, US Dept of Health & Human Services, Public Health Service, NIH, Bethesda, MD 1-1137)

This DNA sequence is then inserted into a bi-cistronic baculovirus vector pAcAB3 (See Figure 22 for the sequence of this vector) along with DNA encoding the corresponding Class II α chain for expression in Sf9 insect cells. This vector can be used to express any Class II HLA-peptide complex in insect cells.

Example 17 Expression and refolding of Class II HLA-DR1- Flu HA complexes

Class II MHC expression is carried out using the bi-cistronic expression vectors produced as described in Examples 15 and 16 containing the Class II HLA-DR1 α and β chains and the Flu HA peptide. The expression and purification methods used are as described in (Gauthier (1998) PNAS USA **95** p11828-11833). Briefly, soluble HLA-DR1 is expressed in the baculovirus system by replacing the hydrophobic transmembrane regions and cytoplasmic segments of DR α and β chains with leucine zipper dimerization domains from the transcription factors Fos and Jun. In the expression construct, the required Class MHC-loaded Flu HA peptide sequence is covalently linked to the N terminus of the mature DR β chain and the DR α chain contains a biotinylation tag sequence to facilitate bifunctional ligand formation utilizing the biotin / strepavidin multimerisation methodology. The recombinant protein is secreted by Sf9 cells infected with the recombinant baculovirus, and purified by affinity chromatography. The protein is further purified by anion-exchange HPLC.

Example 18 –Construction of Class I soluble peptide-HLA molecules

In order to investigate further the specificity of the high affinity A6 TCR clone 134 the following soluble class I peptide-HLA molecules were produced:

HLA-A2 – peptide (LLGRNSFEV)
HLA-A2 – peptide (KLVALGINAV)
HLA-A2 – peptide (LLGDLFGV)
HLA-B8 - peptide (FLRGRAYGL)
HLA-B27 – peptide (HRCQAIRKK)
HLA - Cw6 – peptide (YRSGIIAVV)
HLA-A24 – peptide (VYGFVRACL)
HLA-A2 – peptide (ILAKFLHWL)
HLA-A2 – peptide (LTLGEFLKL)
HLA-A2 – peptide (GILGFVFTL)
HLA-A2 – peptide (SLYNTVATL)

These soluble peptide-HLAs were produced using the methods described in Example 10.

Example 19 – BIAcore surface plasmon resonance measurement of the specificity of a high affinity A6 TCR binding to peptide-HLA.

A surface plasmon resonance biosensor (BIAcore 3000™) was used to analyse the binding specificitiy of the high affinity clone 134 A6 TCR. (See Figures 15a & 15b for the full DNA and amino acid sequences of the mutated TCR β chain respectively) This was carried out using the Class II HLA-DR1-peptide, produced as described in Examples 15 –17, and the Class I peptide-HLA complexes listed in Example 18, produced using the methods detailed in Example 10. The following table lists the peptide-HLA complexes utilised:

1. HLA-A2 – peptide (LLGRNSFEV)
2. HLA-A2 – peptide (KLVALGINAV)
3. HLA-A2 – peptide (LLGDLFGV)
4. HLA-B8 - peptide (FLRGRAYGL)
5. HLA-B27 – peptide (HRCQAIRKK)
6. HLA - Cw6 – peptide (YRSGIIAVV)
7. HLA-A24 – peptide (VYGFVRACL)
8. HLA-A2 – peptide (ILAKFLHWL)
9. HLA-A2 – peptide (LTLGEFLKL)
10. HLA-DR1- peptide (PKYVKQNTLKLA)
11. HLA-A2 – peptide (GILGFVFTL)
12. HLA-A2 – peptide (SLYNTVATL)

The above peptide HLAs were immobilised to streptavidin-coated binding surfaces in of the flow cells of a BIAcore 3000™ in a semi-oriented fashion.

The BIAcore 3000™ allows testing of the binding of the soluble T-cell receptor to up to four different pMHC (immobilised on separate flow cells) simultaneously. For this experiment three different HLA-peptides were immobilised in flowcells 2-4 and flowcell 1 was left blank as a control. Manual injection of HLA-peptide complexes allowed the precise level of immobilised molecules to be manipulated.

After the ability of the high affinity A6 TCR clone 134 to bind to the first 3 HLA-peptide complexes in the above list had been assessed the next three were immobilised onto these flowcells directly on top of the previous ones. This process was continued until the binding of the high affinity A6 TCR clone 134 to all 12 HLA-peptide complexes had been assessed.

Ten injections of 5 µl of the high affinity A6 TCR clone 134 were passed over each flowcell at at 5 µl/min at concentrations ranging from 4.1 ng/ml to 2.1 mg/ml. (See Figures 24-28)

As a final control the high affinity A6 TCR clone 134 was passed over a flowcell containing immobilised HLA-A2 Tax (LLFGYPVYV), the cognate ligand for this TCR.

Specific binding of the high affinity A6 TCR clone 134 was only noted to its cognate ligand. (HLA-A2 Tax (LLFGYPVYV)) These data further demonstrate the specificity of the high affinity A6 TCR clone 134.

Claims:

1. A proteinaceous particle displaying on its surface a T-cell receptor (TCR), characterised in that

(i) the proteinaceous particle is a ribosome and the TCR is a single chain TCR (scTCR) polypeptide, or

(ii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a human scTCR or a human dimeric T-cell receptor (dTCR) polypeptide pair, or

(iii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a non-human dTCR polypeptide pair, or

(iv) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a scTCR polypeptide comprising TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain, and a disulfide bond which has no equivalent in native T cell receptors links residues of the constant region sequences.

2. A proteinaceous particle, displaying on its surface a dimeric T-cell receptor (dTCR) polypeptide pair, or a single chain T-cell receptor (scTCR) polypeptide wherein.

the dTCR polypeptide pair is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains,

and the scTCR is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain;

the variable region sequences of the dTCR polypeptide pair or scTCR polypeptide are mutually orientated substantially as in native TCRs; and

in the case of the scTCR polypeptide a disulfide bond which has no equivalent in native T cell receptors links residues of the polypeptide.

3. A proteinaceous particle as claimed in claim 1 or claim 2, which is a phage particle.

4. A proteinaceous particle as claimed in claim 1 or claim 2, which is a cell surface protein or polypeptide.

5. A proteinaceous particle as claimed in claim 1 or claim 2, which is a ribosome.

6. A proteinaceous particle as claimed in any of the preceding claims wherein the C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a peptide bond to a surface exposed residue of the proteinaceous particle.

7. A proteinaceous particle as claimed in any of claims 1 to 4 wherein the C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a disulfide bond to a surface exposed cysteine residue of the proteinaceous particle.

8. A proteinaceous particle as claimed in any of the preceding claims wherein an scTCR polypeptide is displayed which comprises

a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region

a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR β chain constant region extracellular sequence, and

a linker sequence linking the C terminus of the first segment to the N terminus of the second segment.

9. A proteinaceous particle as claimed in any of claims 1 to 7 wherein an scTCR polypeptide is displayed which comprises

a first segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region

a second segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence, and

a linker sequence linking the C terminus of the first segment to the N terminus of the second segment.

10. A proteinaceous particle as claimed in any of claims 1 to 7 wherein a scTCR polypeptide is displayed which has

a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence,

a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region fused to the N terminus of an amino acid sequence corresponding to TCR β chain constant region extracellular sequence,

a linker sequence linking the C terminus of the first segment to the N terminus of the second segment, or vice versa, and

a disulfide bond between the first and second chains, said disulfide bond being one which has no equivalent in native αβ or γδ T cell receptors,

the length of the linker sequence and the position of the disulfide bond being such that the variable region sequences of the first and second segments are mutually orientated substantially as in native αβ or γδ T cell receptors.

11. A proteinaceous particle as claimed in claim 10 wherein the linker sequence has the formula -P-AA-P- wherein P is proline and AA represents an amino acid sequence wherein the amino acids are glycine and serine.

12. A proteinaceous particle as claimed in claim 10 or claim 11 wherein the linker sequence links the C terminus of the first segment to the N terminus of the second segment.

13. A proteinaceous particle as claimed in claim 12 wherein the linker sequence consists of from 26 to 41 amino acids.

14. A proteinaceous particle as claimed in claim 13 wherein the linker sequence consists of 29, 30, 31 or 32 amino acids.

15. A proteinaceous particle as claimed in claim 13 wherein the linker sequence consists of 33, 34, 35 or 36 amino acids.

16. A proteinaceous particle as claimed in claim 13 wherein the linker sequence has the formula -PGGG-$(SGGGG)_5$-P- wherein P is proline, G is glycine and S is serine.

17. A proteinaceous particle as claimed in claim 13 wherein the linker sequence has the formula -PGGG-$(SGGGG)_6$-P- wherein P is proline, G is glycine and S is serine.

18. A proteinaceous particle as claimed in any of claims 1 to 4, 6 or 7 wherein a dTCR polypeptide pair is displayed which is constituted by

a first polypeptide wherein a sequence corresponding to a TCR α or δ chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant region extracellular sequence, and

a second polypeptide wherein a sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus a sequence corresponding to a TCR β chain constant region extracellular sequence,

the first and second polypeptides being linked by a disulfide bond which has no equivalent in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

19. A proteinaceous particle as claimed in any preceding claim wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to $\alpha\beta$ TCR extracellular constant and variable region sequences.

20. A proteinaceous particle as claimed in any of claims 1 to 18 wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to extracellular αβ TCR constant region sequences and γδ TCR variable region sequences.

21. A proteinaceous particle as claimed in any preceding claim wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to non-human extracellular αβ TCR constant region sequences and human TCR variable region sequences.

22. A proteinaceous particle as claimed in any of the preceding claims wherein an amino acid sequence of one member of the displayed dTCR polypeptide pair, or an amino acid sequence of the displayed scTCR, corresponds to a native TCR extracellular constant chain Ig domain sequence.

23. A proteinaceous particle as claimed in any of the preceding claims wherein the displayed dTCR polypeptide pair or displayed scTCR, includes sequences corresponding to native TCR extracellular constant chain Ig domain sequences.

24. A proteinaceous particle as claimed in claim 23 wherein a disulfide bond links amino acid residues of the said constant chain Ig domain sequences, which disulfide bond has no equivalent in native TCRs.

25. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues corresponding to amino acid residues whose β carbon atoms are less than 0.6 nm apart in native TCRs.

26. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 48 of exon 1 of TRAC*01 and Ser 57 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

27. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 45 of exon 1 of TRAC*01 and Ser 77 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

28. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Tyr 10 of exon 1 of TRAC*01 and Ser 17 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

29. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 45 of exon 1 of TRAC*01 and Asp 59 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

30. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Ser 15 of exon 1 of TRAC*01 and Glu 15 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

31. A proteinaceous particle as claimed in any of claims 23 to 30 wherein the sequences corresponding to native TCR extracellular constant chain Ig domain sequences are truncated at their C-termini relative to said native sequences such that the cysteine residues which form the native interchain disulphide bond are excluded.

32. A proteinaceous particle as claimed in any of claims 23 to 30 wherein in the sequences corresponding to native TCR extracellular constant chain Ig domain sequences the cysteine residues which form the native interchain disulphide bond are substituted by non-cysteine residues.

33. A proteinaceous particle as claimed in claim 32 wherein the cysteine residues which form the native interchain disulfide bond are substituted by serine or alanine.

34. A proteinaceous particle as claimed in any of the preceding claims wherein in the displayed dTCR or scTCR there is no unpaired cysteine residue corresponding an unpaired cysteine residue present in a native TCR.

35. A proteinaceous particle as claimed in any of claims 23 to 34 wherein the sequences corresponding to native TCR extracellular constant chain Ig domain sequences are truncated N-terminal to residues corresponding to those which form the non-native interchain disulphide bond.

36. A diverse library of dTCR polypeptide pairs or scTCR polypeptides displayed on proteinaceous particles said dTCR polypeptide pairs or scTCR polypeptides having the structural features defined in any of claims 8 to 35.

37. A diverse library as claimed in claim 36 wherein the diversity resides in the variable region(s) of the dTCR or scTCR polypeptides.

38. A diverse library as claimed in claim 36 wherein the diversity resides in one or more of the complementarity determining regions of the variable region(s) of the dTCR or scTCR polypeptides.

39. A diverse library as claimed in any of claims 36 to 38 wherein the dTCR or scTCR polypeptides are displayed on phage particles.

40. Nucleic acid encoding (a) one chain of a dTCR polypeptide pair and (b) the other chain of a dTCR polypeptide pair fused to a nucleic acid sequence encoding a particle forming protein, or nucleic acid encoding a scTCR polypeptide fused to a nucleic acid sequence encoding a particle forming protein, the dTCR pair or scTCR having the structural features defined in any of claims 8 to 35.

41. An expression vector comprising nucleic acid as claimed in claim 40.

42. An expression vector as claimed in claim 41 which is a phagemid or phage genome vector.

43. A phagemid or phage genome vector as claimed in claim 42 wherein the nucleic acid sequence(s) which encode the particle-forming protein is (are) derived from a filamentous phage.

44. A phagemid or phage genome vector as claimed in claim 43 wherein the said nucleic acid sequence(s) encode(s) bacteriophage gIII or gVIII coat proteins.

45. An expression vector as claimed in any of claims 41 to 44 containing a sequence or sequences which limit constitutively or inducibly the amount of TCR polypeptide expressed by the vector to a desired level.

46. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) weak promoter sequence(s)

47. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) mutated ribosome binding site(s).

48. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) miss-sense suppressor stop codon(s).

49. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) mutated start codon(s).

50. An expression vector as claimed in claim 45 wherein the said sequence(s) contain(s) a number of codons less preferred by the expression system being utilised.

51. A host cell comprising nucleic acid as claimed in claim 40, or an expression vector as claimed in any of claims 41 to 50.

52. A host cell harbouring a phagemid expression vector as claimed in any of claims 42 to 50, and a helper phage.

53. A method for the identification of TCRs with a specific characteristic, said method comprising subjecting a diverse library of TCRs displayed on proteinaceous particles as claimed in any of claims 36 to 39 to an assay which measures said characteristic, identifying those proteinaceous particles which display a TCR with the desired characteristic and isolating these proteinaceous particles.

54. A method as claimed in claim 53 wherein the specific characteristic is increased affinity for a TCR ligand.

55. A method for detecting TCR ligand complexes, which comprises:

(i) providing a TCR-displaying proteinaceous particle as claimed in any of claims 1 to 39;

(ii) contacting said TCR-displaying proteinaceous particle with a putative ligand complex; and

(iii) detecting binding of the said TCR-displaying proteinaceous particle to the putative ligand complexes.

56 A method as claimed in claim 55 wherein the putative TCR ligand complexes are peptide-MHC complexes.

57. A method of identifying an inhibitor of the interaction between a TCR-displaying proteinaceous particle as claimed in any one of claims 1 to 39, and a TCR-binding ligand comprising contacting the TCR-displaying proteinaceous particle with a TCR-binding ligand, in the presence of and in the absence of a test compound, and determining whether the presence of the test compound reduces binding of the TCR-

displaying proteinaceous particle to the TCR-binding ligand, such reduction being taken as identifying an inhibitor.

58. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has a Kd for the said TCR ligand less than that of the native TCR.

59. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has a Kd for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

60. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR

61. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

62. A dimeric TCR as claimed in any of claims 58 to 61 which has the structural features of an αβ heterodimeric TCR defined in any of claims 18 to 35.

63. A TCR as claimed in any of claims 58 to 62 which is mutated relative to the native TCR in at least one complementarity determining region.

64. A TCR as claimed in any of claims 58 to 63 which is specific for a given MHC type or types.

65. A TCR as claimed in any of claims 58 to 63 which is specific for a given pMHC.

66. A TCR as claimed in any of claims 58 to 63 or 65 which is specific for the HLA-A2 Tax peptide (LLFGYPVYV) complex.

67. A TCR as claimed in any of claims 58 to 66 associated with a therapeutic or imaging compound.

68. A TCR as claimed in any of claims 58 to 66 associated with a cytotoxic compound.

69. A TCR as claimed in claim 68 wherein the TCR is specific for the HLA-A2 Tax peptide (LLFGYPVYV) complex.

70. A method of treatment of HTLV-1 infection comprising administering to a subject suffering such infection an effective amount of a TCR as claimed in claim 66 or claim 68.

71. The use of a TCR as claimed in claim 66 or claim 68 in the preparation of a composition for the treatment of HTLV-1 infection.

Figure 1a

atgcagaaggaagtggagcagaactctggacccctcagtgttccagagggagccatt
gcctctctcaactgcacttacagtgaccgaggttcccagtccttcttctggtacaga
caatattctgggaaaagccctgagttgataatgtccatatactccaatggtgacaaa
gaagatggaaggtttacagcacagctcaataaagccagccagtatgtttctctgctc
atcagagactcccagcccagtgattcagccacctacctctgtgccgttacaactgac
agctgggggaaattgcagtttggagcagggacccaggttgtggtcaccccagatatc
cagaaccctgaccctgccgtgtaccagctgagagactctaaatccagtgacaagtct
gtctgcctattcaccgattttgattctcaaacaaatgtgtcacaaagtaaggattct
gatgtgtatatcacagacaaaactgtgctagacatgaggtctatggacttcaagagc
aacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaac
aacagcattattccagaagacaccttcttccccagcccagaaagttcctaa

Figure 1b

atgaacgctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagc
atgacactgcagtgtgcccaggatatgaaccatgaatacatgtcctggtatcgacaa
gacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgac
caaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccg
ctcaggctgctgtcggctgctccctcccagacatctgtgtacttctgtgccagcagg
ccgggactagcgggagggcgaccagagcagtacttcgggccgggcaccaggctcacg
gtcacagaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatca
gaagcagagatctcccacacccaaaaggccacactggtgtgcctggccacaggcttc
taccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggg
gtctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatac
gctctgagcagccgcctgagggtctcggccaccttctggcaggacccccgcaaccac
ttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccaggat
agggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaa

Figure 2a

MQ
K_1EVEQNSGPL SVPEGAIASL NCTYSDRGSQ SFFWYRQYSG KSPELIMSIY
SNGDKEDGRF TAQLNKASQY VSLLIRDSQP SDSATYLCAV TTDSWGKLQF
GAGTQVVVTP DIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS
DVYITDKCVL DMRSMDFKSN SAVAWSNKSD FACANAFNNS IIPEDTFFPS
PESS*

Figure 2b

M
N_1AGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV
GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF CASRPGLAGG
RPEQYFGPGT RLTVTEDLKN VFPPEVAVFE PSEAEISHTQ KATLVCLATG
FYPDHVELSW WVNGKEVHSG VCTDPQPLKE QPALNDSRYA LSSRLRVSAT
FWQDPRNHFR CQVQFYGLSE NDEWTQDRAK PVTQIVSAEA WGRAD*

Figure 3

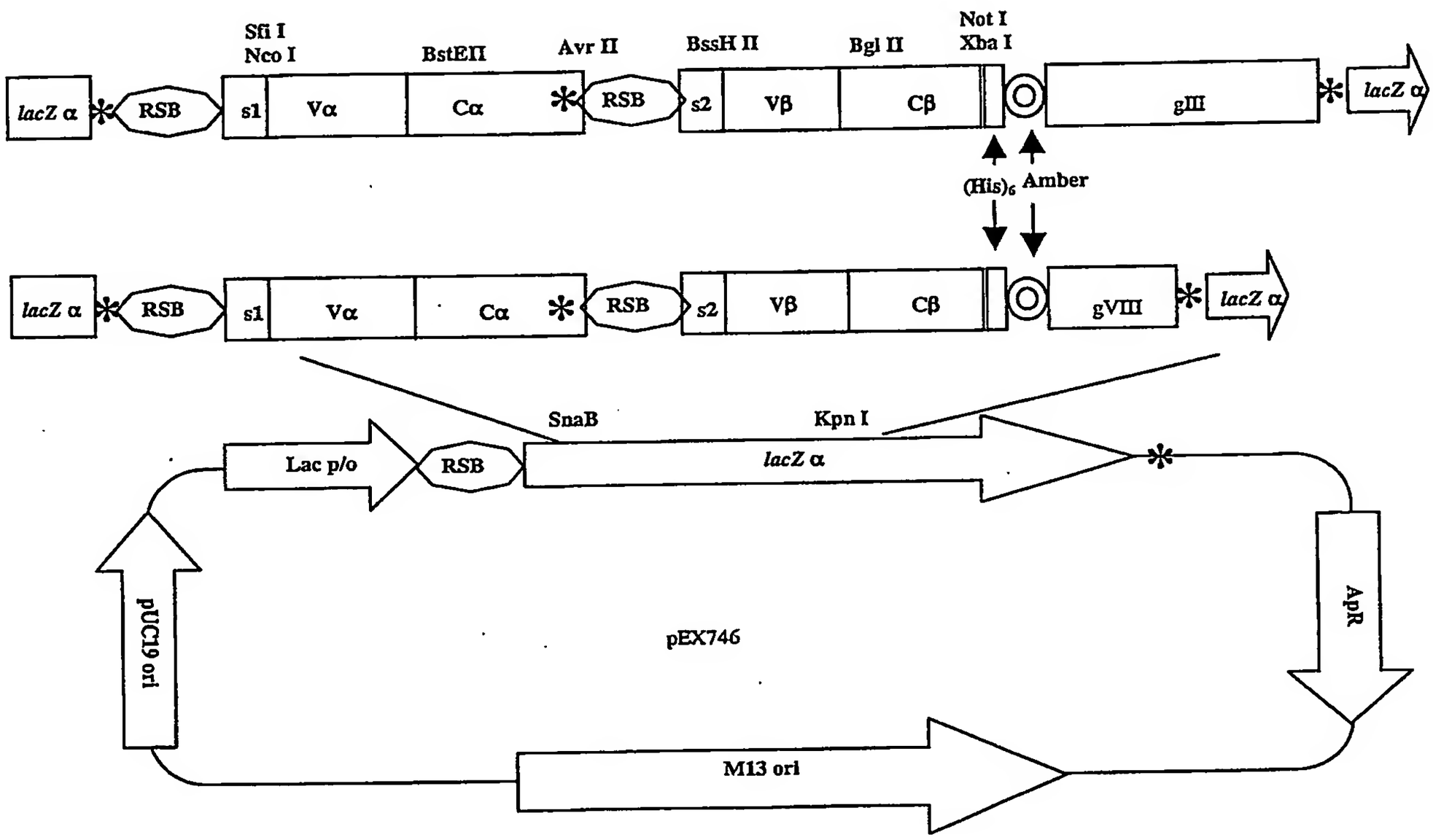

Sfi I
Nco I
BstEII
Avr II
BssH II
Bgl II
Not I
Xba I
lacZ α
RSB
s1
Vα
Cα
RSB
s2
Vβ
Cβ
gIII
lacZ α
(His)6
Amber
gVIII
SnaB
Kpn I
Lac p/o
pUC19 ori
pEX746
ApR
M13 ori

Figure 4

```
   1 gttaactacg tcaggtggca cttttcgggg aaatgtgcgc ggaaccccta tttgtttatt
  61 tttctaaata cattcaaata tgtatccgct catgagacaa taaccctgat aaatgcttca
 121 ataatattga aaaaggaaga gtatgagtat tcaacatttc cgtgtcgccc ttattccctt
 181 ttttgcggca ttttgccttc ctgtttttgc tcacccagaa acgctggtga aagtaaaaga
 241 tgctgaagat cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa
 301 gatccttgag agttttcgcc ccgaagaacg ttctccaatg atgagcactt ttaaagttct
 361 gctatgtggc gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat
 421 acactattct cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga
 481 tggcatgaca gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc
 541 caacttactt ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat
 601 gggggatcat gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa
 661 cgacgagcgt gacaccacga tgcctgtagc aatggcaaca acgttgcgca aactattaac
 721 tggcgaacta cttactctag cttcccggca acaattaata gactggatgg aggcggataa
 781 agttgcagga ccacttctgc gctcggccct tccggctggc tggtttattg ctgataaatc
 841 tggagccggt gagcgtgggt ctcgcggtat cattgcagca ctggggccag atggtaagcc
 901 ctcccgtatc gtagttatct acacgacggg gagtcaggca actatggatg aacgaaatag
 961 acagatcgct gagataggtg cctcactgat taagcattgg taactgtcag accaagttta
1021 ctcatatata ctttagattg atttaccccg gttgataatc agaaaagccc caaaaacagg
1081 aagattgtat aagcaaatat ttaaattgta aacgttaata ttttgttaaa attcgcgtta
1141 aatttttgtt aaatcagctc atttttttaac caataggccg aaatcggcaa aatcccttat
1201 aaatcaaaag aatagcccga gatagggttg agtgttgttc cagtttggaa caagagtcca
1261 ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc
1321 ccactacgtg aaccatcacc caaatcaagt tttttggggt cgaggtgccg taaagcacta
1381 aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcg aacgtggcga
1441 gaaaggaagg gaagaaagcg aaaggagcgg gcgctagggc gctggcaagt gtagcggtca
1501 cgctgcgcgt aaccaccaca cccgccgcgc ttaatgcgcc gctacagggc gcgtaaaagg
1561 atctaggtga agatcctttt tgataatctc atgaccaaaa tcccttaacg tgagttttcg
1621 ttccactgag cgtcagaccc cgtagaaaag atcaaaggat cttcttgaga tccttttttt
1681 ctgcgcgtaa tctgctgctt gcaaacaaaa aaaccaccgc taccagcggt ggtttgtttg
1741 ccggatcaag agctaccaac tctttttccg aaggtaactg gcttcagcag agcgcagata
1801 ccaaatactg ttcttctagt gtagccgtag ttaggccacc acttcaagaa ctctgtagca
1861 ccgcctacat acctcgctct gctaatcctg ttaccagtgg ctgctgccag tggcgataag
1921 tcgtgtctta ccgggttgga ctcaagacga tagttaccgg ataaggcgca gcggtcgggc
1981 tgaacggggg gttcgtgcac acagcccagc ttggagcgaa cgacctacac cgaactgaga
2041 tacctacagc gtgagctatg agaaagcgcc acgcttcccg aagggagaaa ggcggacagg
2101 tatccggtaa gcggcagggt cggaacagga gagcgcacga gggagcttcc agggggaaac
2161 gcctggtatc tttatagtcc tgtcgggttt cgccacctct gacttgagcg tcgatttttg
2221 tgatgctcgt caggggggcg gagcctatgg aaaaacgcca gcaacgcggc ctttttacgg
2281 ttcctggcct tttgctggcc ttttgctcac atgtaatgtg agttagctca ctcattaggc
2341 accccaggct ttacacttta tgcttccggc tcgtatgttg tgtggaattg tgagcggata
2401 acaatttcac acaggaaaca gctatgacca tgattacgcc aagctacgta taataatatt
2461 ctatttcaag gagacagtca taatgaaata cctattgcct acggcagccg ctggattgtt
2521 attactcgcg gcccagccgg ccatggccca gaaggaagtg gagcagaact ctggacccct
2581 cagtgttcca gagggagcca ttgcctctct caactgcact tacagtgacc gaggttccca
2641 gtccttcttc tggtacagac aatattctgg gaaaagccct gagttgataa tgtccatata
2701 ctccaatggt gacaaagaag atggaaggtt tacagcacag ctcaataaag ccagccagta
2761 tgtttctctg ctcatcagag actcccagcc cagtgattca gccacctacc tctgtgccgt
2821 tacaactgac agctggggga aattgcagtt tggagcaggg acccaggttg tggtcacccc
2881 agatatccag aaccctgacc ctgccgtgta ccagctgaga gactctaaat ccagtgacaa
2941 gtctgtctgc ctattcaccg attttgattc tcaaacaaat gtgtcacaaa gtaaggattc
3001 tgatgtgtat atcacagaca aatgtgtgct agacatgagg tctatggact tcaagagcaa
3061 cagtgctgtg gcctggagca acaaatctga ctttgcatgt gcaaacgcct tcaacaacag
3121 cattattcca gaagacacct tcttccccag cccagaaagt tcctaataac ctaggttaat
3181 taagaattct ttaagaagga gatatacata tgaaaaaatt attattcgca attcctttag
3241 ttgttccttt ctattctcac agcgcgcagg ctggtgtcac tcagacccca aaattccagg
3301 tcctgaagac aggacagagc atgacactgc agtgtgccca ggatatgaac catgaataca
3361 tgtcctggta tcgacaagac ccaggcatgg ggctgaggct gattcattac tcagttggtg
```

3421 ctggtatcac tgaccaagga gaagtcccca atggctacaa tgtctccaga tcaaccacag
3481 aggatttccc gctcaggctg ctgtcggctg ctccctccca gacatctgtg tacttctgtg
3541 ccagcaggcc gggactagcg ggagggcgac cagagcagta cttcgggccg ggcaccaggc
3601 tcacggtcac agaggacctg aaaaacgtgt tcccacccga ggtcgctgtg tttgagccat
3661 cagaagcaga gatctcccac acccaaaagg ccacactggt gtgcctggcc acaggcttct
3721 accccgacca cgtggagctg agctggtggg tgaatgggaa ggaggtgcac agtggggtct
3781 gcacagaccc gcagcccctc aaggagcagc ccgccctcaa tgactccaga tacgctctga
3841 gcagccgcct gagggtctcg gccaccttct ggcaggaccc ccgcaaccac ttccgctgtc
3901 aagtccagtt ctacgggctc tcggagaatg acgagtggac ccaggatagg gccaaacccg
3961 tcacccagat cgtcagcgcc gaggcctggg gtagagcaga cgcggccgca tctagacatc
4021 atcaccatca tcactagact gttgaaagtt gtttagcaaa accccataca gaaaattcat
4081 ttactaacgt ctggaaagac gacaaaactt tagatcgtta cgctaactat gagggttgtc
4141 tgtggaatgc tacaggcgtt gtagtttgta ctggtgacga aactcagtgt tacggtacat
4201 gggttcctat tgggcttgct atccctgaaa atgagggtgg tggctctgag ggtggcggtt
4261 ctgagggtgg cggttctgag ggtggcggta ctaaacctcc tgagtacggt gatacaccta
4321 ttccgggcta tacttatatc aaccctctcg acggcactta tccgcctggt actgagcaaa
4381 accccgctaa tcctaatcct tctcttgagg agtctcagcc tcttaatact ttcatgtttc
4441 agaataatag gttccgaaat aggcaggggg cattaactgt ttatacgggc actgttactc
4501 aaggcactga ccccgttaaa acttattacc agtacactcc tgtatcatca aaagccatgt
4561 atgacgctta ctggaacggt aaattcagag actgcgcttt ccattctggc tttaatgagg
4621 atccattcgt ttgtgaatat caaggccaat cgtctgacct gcctcaacct cctgtcaatg
4681 ctggcggcgg ctctggtggt ggttctggtg gcggctctga gggtggtggc tctgagggtg
4741 gcggttctga gggtggcggc tctgagggag gcggttccgg tggtggctct ggttccggtg
4801 attttgatta tgaaaagatg gcaaacgcta ataaggggggc tatgaccgaa aatgccgatg
4861 aaaacgcgct acagtctgac gctaaaggca aacttgattc tgtcgctact gattacggtg
4921 ctgctatcga tggtttcatt ggtgacgttt ccggccttgc taatggtaat ggtgctactg
4981 gtgattttgc tggctctaat tcccaaatgg ctcaagtcgg tgacggtgat aattcacctt
5041 taatgaataa tttccgtcaa tatttacctt ccctccctca atcggttgaa tgtcgccctt
5101 ttgtctttag cgctggtaaa ccatatgaat tttctattga ttgtgacaaa ataaacttat
5161 tccgtggtgt ctttgcgttt cttttatatg ttgccacctt tatgtatgta ttttctacgt
5221 ttgctaacat actgcgtaat aaggagtctt aataaggtac cctctagtca aggcctatag
5281 tgagtcgtat tacggactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt
5341 tacccaactt aatcgccttg cagcacatcc ccctttcgcc agctggcgta atagcgaaga
5401 ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat ggcgcttcgc
5461 ttggtaataa agcccgcttc ggcgggcttt ttttt

Figure 5

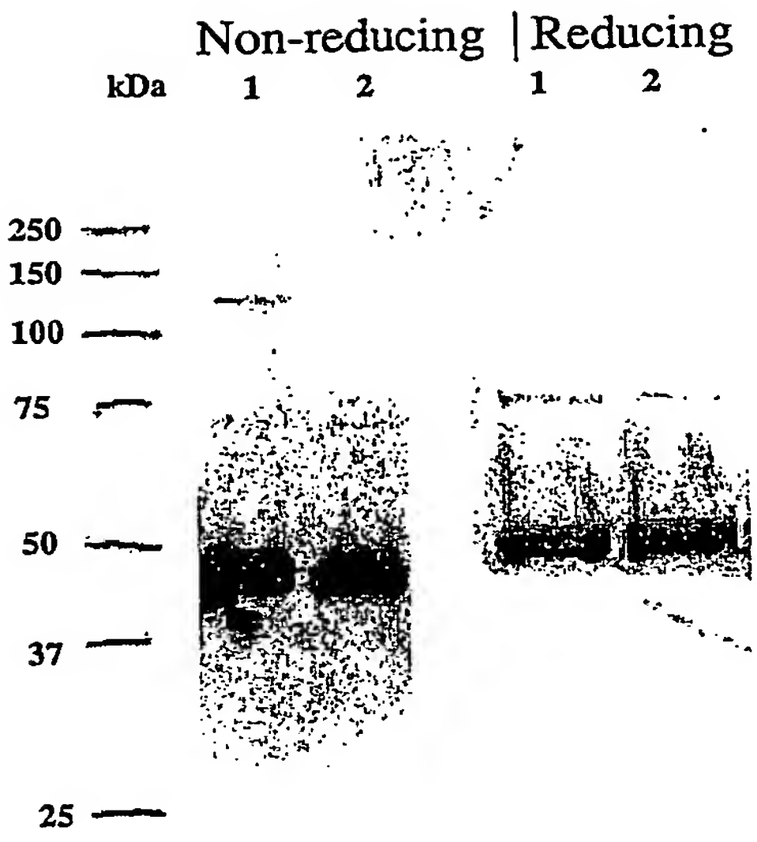


Figure 6

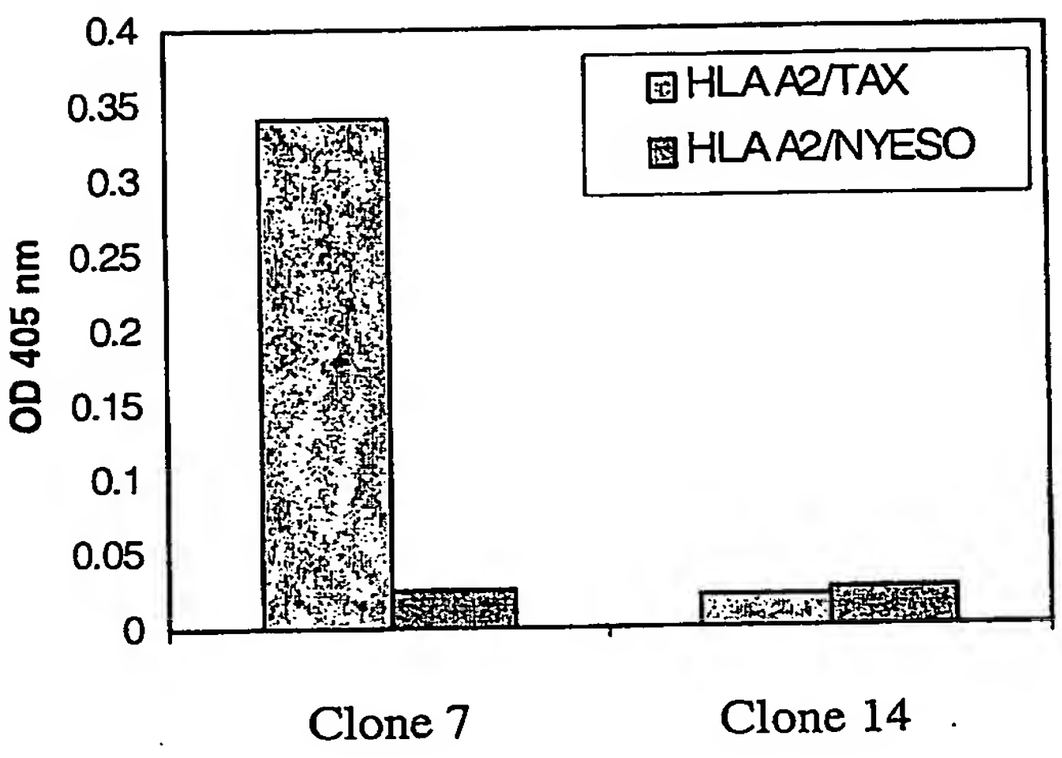

0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
OD 405 nm
HLA A2/TAX
HLA A2/NYESO
Clone 7
Clone 14

Figure 7a

Schematic diagram of the A6 scTCR-C-Kappa ribosome display construct

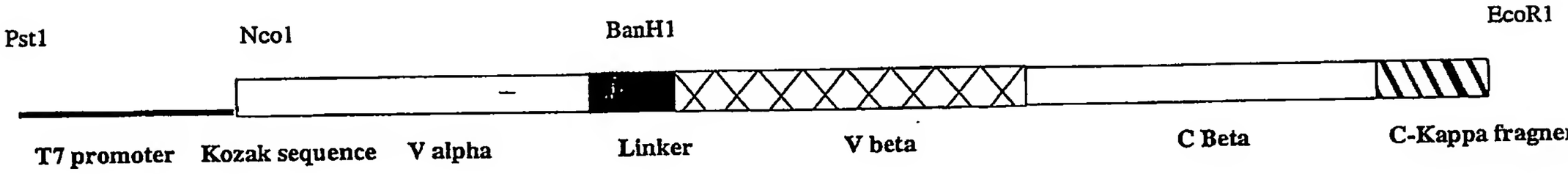
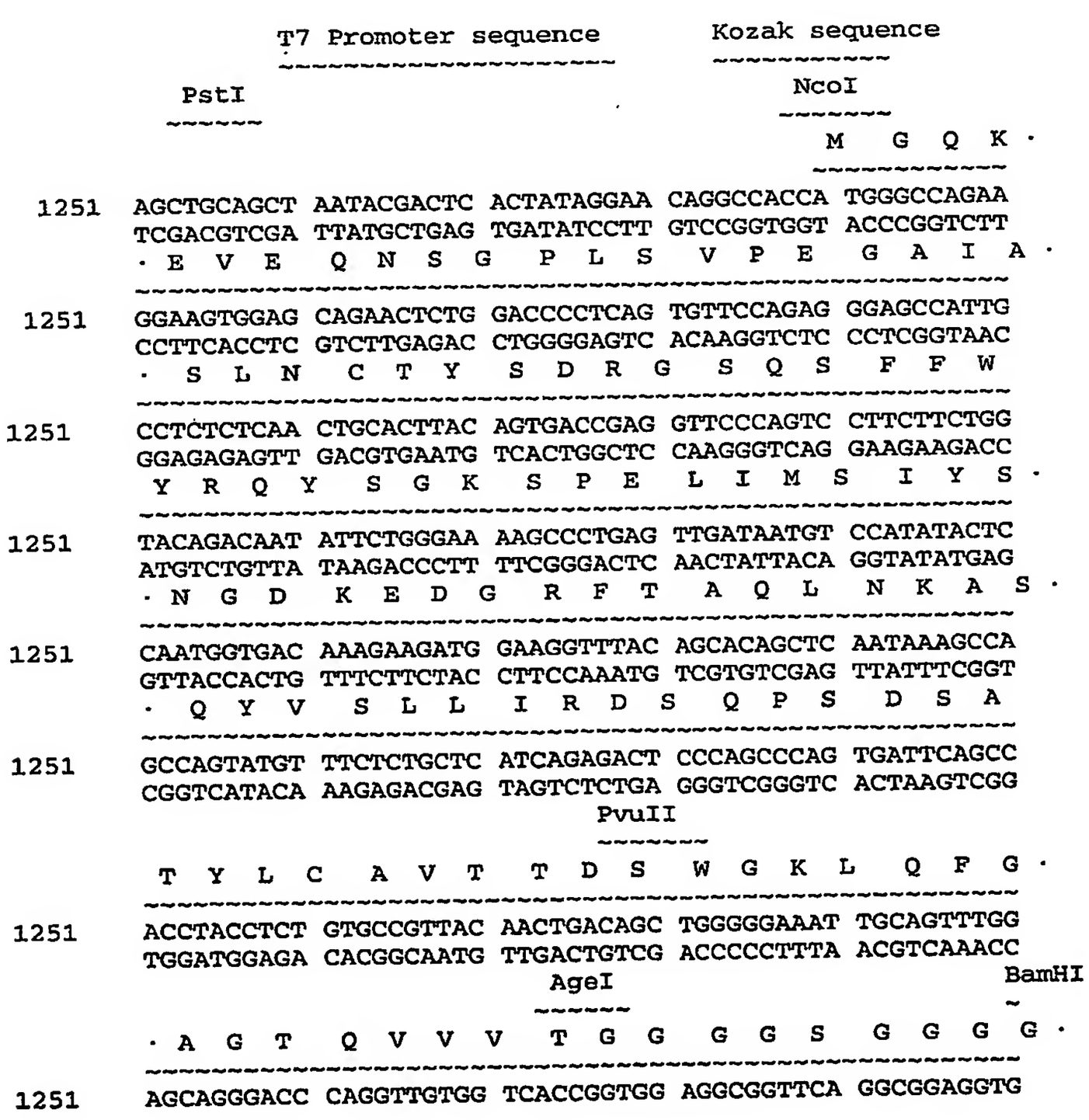


Figure 7b



```
          TCGTCCCTGG GTCCAACACC AGTGGCCACC TCCGCCAAGT CCGCCTCCAC
          BamHI
          ------
          .  S  G  G   G  G  S   N  A  G  V   T  Q  T   P  K  F
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GATCCGGCGG TGGCGGGTCG AACGCTGGTG TCACTCAGAC CCCAAAATTC
          CTAGGCCGCC ACCGCCCAGC TTGCGACCAC AGTGAGTCTG GGGTTTTAAG
                                          PstI
                                          ------
           Q  V  L  K   T  G  Q   S  M  T   L  Q  C  A   Q  D  M  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      CAGGTCCTGA AGACAGGACA GAGCATGACA CTGCAGTGTG CCCAGGATAT
          GTCCAGGACT TCTGTCCTGT CTCGTACTGT GACGTCACAC GGGTCCTATA
          .  N  H  E   Y  M  S  W   Y  R  Q   D  P  G   M  G  L  R  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GAACCATGAA TACATGTCCT GGTATCGACA AGACCCAGGC ATGGGGCTGA
          CTTGGTACTT ATGTACAGGA CCATAGCTGT TCTGGGTCCG TACCCCGACT
          .  L  I  H   Y  S  V   G  A  G  I   T  D  Q   G  E  V
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GGCTGATTCA TTACTCAGTT GGTGCTGGTA TCACTGACCA AGGAGAAGTC
          CCGACTAAGT AATGAGTCAA CCACGACCAT AGTGACTGGT TCCTCTTCAG
           P  N  G  Y   N  V  S   R  S  T   T  E  D  F   P  L  R  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      CCCAATGGCT ACAATGTCTC CAGATCAACC ACAGAGGATT TCCCGCTCAG
          GGGTTACCGA TGTTACAGAG GTCTAGTTGG TGTCTCCTAA AGGGCGAGTC
          .  L  L  S   A  A  P  S   Q  T  S   V  Y  F   C  A  S  R  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GCTGCTGTCG GCTGCTCCCT CCCAGACATC TGTGTACTTC TGTGCCAGCA
          CGACGACAGC CGACGAGGGA GGGTCTGTAG ACACATGAAG ACACGGTCGT
                                          ScaI
                                          ------
          .  P  G  L   A  G  G   R  P  E  Q   Y  F  G   P  G  T
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GGCCGGGACT AGCGGGAGGG CGACCAGAGC AGTACTTCGG GCCGGGCACC
          CCGGCCCTGA TCGCCCTCCC GCTGGTCTCG TCATGAAGCC CGGCCCGTGG
           R  L  T  V   T  E  D   L  K  N   V  F  P  P   E  V  A  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      AGGCTCACGG TCACAGAGGA CCTGAAAAAC GTGTTCCCAC CCGAGGTCGC
          TCCGAGTGCC AGTGTCTCCT GGACTTTTTG CACAAGGGTG GGCTCCAGCG
                                  BglII
                                  ------
          .  V  F  E   P  S  E  A   E  I  S   H  T  Q   K  A  T  L  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      TGTGTTTGAG CCATCAGAAG CAGAGATCTC CCACACCCAA AAGGCCACAC
          ACACAAACTC GGTAGTCTTC GTCTCTAGAG GGTGTGGGTT TTCCGGTGTG
          .  V  C  L   A  T  G   F  Y  P  D   H  V  E   L  S  W
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      TGGTGTGCCT GGCCACAGGC TTCTACCCCG ACCACGTGGA GCTGAGCTGG
          ACCACACGGA CCGGTGTCCG AAGATGGGGC TGGTGCACCT CGACTCGACC
                              ApaLI
                              -------
           W  V  N  G   K  E  V   H  S  G   V  S  T  D   P  Q  P  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      TGGGTGAATG GGAAGGAGGT GCACAGTGGG GTCAGCACAG ACCCGCAGCC
          ACCCACTTAC CCTTCCTCCA CGTGTCACCC CAGTCGTGTC TGGGCGTCGG
          .  L  K  E   Q  P  A  L   N  D  S   R  Y  A   L  S  S  R  .
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      CCTCAAGGAG CAGCCCGCCC TCAATGACTC CAGATACGCT CTGAGCAGCC
          GGAGTTCCTC GTCGGGCGGG AGTTACTGAG GTCTATGCGA GACTCGTCGG
           Bsu36I
           -------
          .  L  R  V   S  A  T   F  W  Q  D   P  R  N   H  F  R
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251      GCCTGAGGGT CTCGGCCACC TTCTGGCAGG ACCCCCGCAA CCACTTCCGC
          CGGACTCCCA GAGCCGGTGG AAGACCGTCC TGGGGGCGTT GGTGAAGGCG
           C  Q  V  Q   F  Y  G   L  S  E   N  D  E  W   T  Q  D  .
```

```
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251            TGTCAAGTCC AGTTCTACGG GCTCTCGGAG AATGACGAGT GGACCCAGGA
                ACAGTTCAGG TCAAGATGCC CGAGAGCCTC TTACTGCTCA CCTGGGTCCT
                                                  StuI
                                                  ~~~~~~~
                · R  A  K   P  V  T  Q   I  V  S   A  E  A   W  G  R  A ·
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251            TAGGGCCAAA CCCGTCACCC AGATCGTCAG CGCCGAGGCC TGGGGTAGAG
                ATCCCGGTTT GGGCAGTGGG TCTAGCAGTC GCGGCTCCGG ACCCCATCTC
                · D  G  G   G  G  S   L  S  S  T   L  T  L   S  K  A
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251            CAGACGGTGG AGGCGGTTCA CTCAGCAGCA CCCTGACGCT GAGCAAAGCA
                GTCTGCCACC TCCGCCAAGT GAGTCGTCGT GGGACTGCGA CTCGTTTCGT
                 D  Y  E  K   H  K  V   Y  A  C   E  V  T  H   Q  G  L ·
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251            GACTACGAGA AACACAAAGT CTACGCCTGC GAAGTCACCC ATCAGGGCCT
                CTGATGCTCT TTGTGTTTCA GATGCGGACG CTTCAGTGGG TAGTCCCGGA
                                                                EcoRI
                                                                ~~~~~~
                · S  S  P   V  T  K  S   F  N  R   G  E  S
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1251            GAGTTCGCCC GTCACAAAGA GCTTCAACCG CGGAGAGTCA TAAGAATTCT
                CTCAAGCGGG CAGTGTTTCT CGAAGTTGGC GCCTCTCAGT ATTCTTAAGA
1251            CAG
                GTC
```

Figure 8

pUC19-T7 sequence

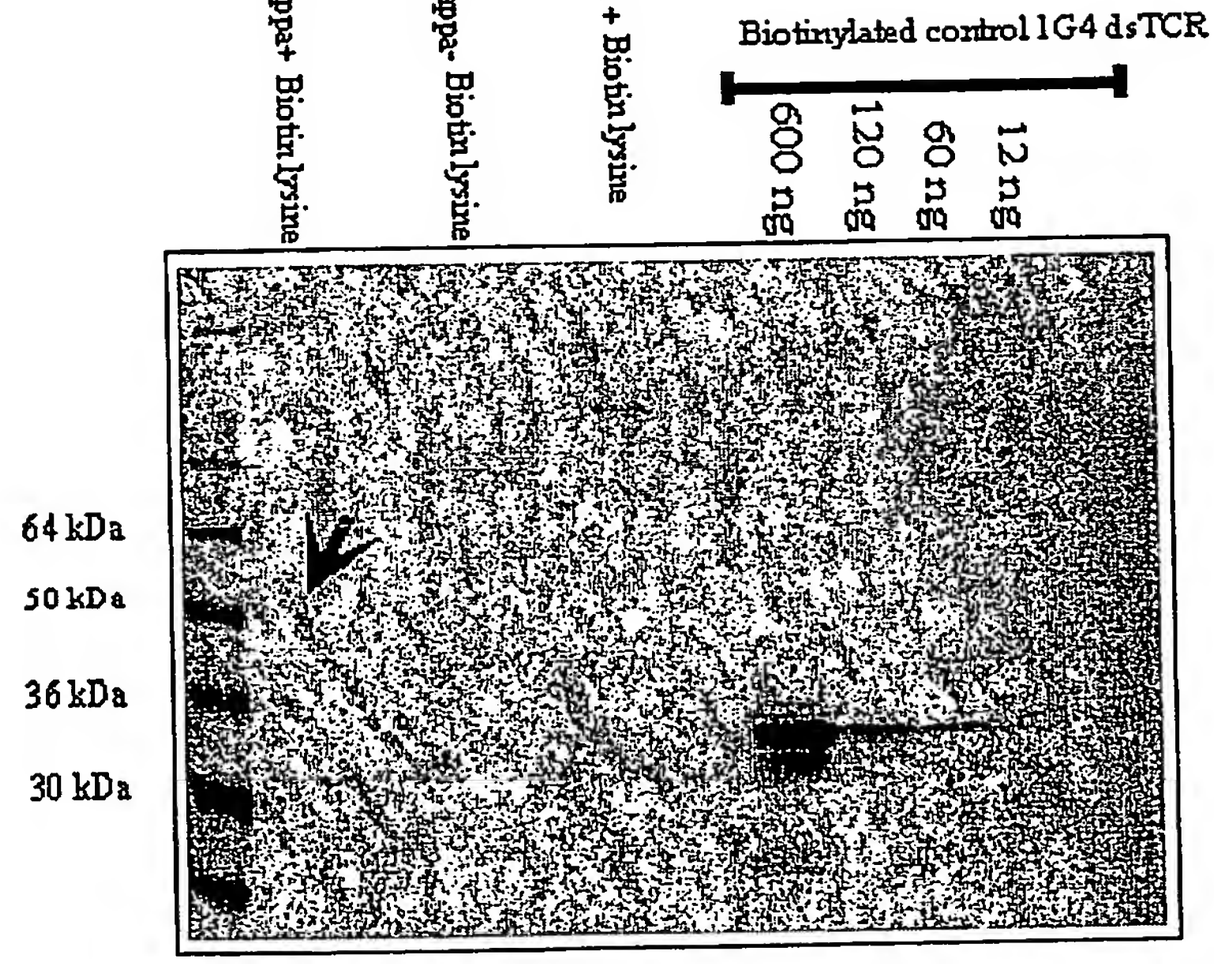
```
   1 ctgctttccc ggagcactat gcggataaaa atatccaatt acagtactat tattaccaaa gaatctgcag
  71 tccaccgtga aaagcccctt tacacgcgcc ttggggataa acaaataaaa agatttatgt aagtttatac
 141 ataggcgagt actctgttat tgggactatt tacgaagtta ttataacttt ttccttctca tactcataag
 211 ttgtaaaggc acagcgggaa taagggaaaa aacgccgtaa aacggaagga caaaaacgag tgggtctttg
 281 cgaccacttt cattttctac gacttctagt caacccacgt gctcacccaa tgtagcttga cctagagttg
 351 tcgccattct aggaactctc aaaagcgggg cttcttgcaa aaggttacta ctcgtgaaaa tttcaagacg
 421 atacaccgcg ccataatagg gcataactgc ggcccgttct cgttgagcca gcggcgtatg tgataagagt
 491 cttactgaac caactcatga gtggtcagtg tcttttcgta gaatgcctac cgtactgtca ttctcttaat
 561 acgtcacgac ggtattggta ctcactattg tgacgccggt tgaatgaaga ctgttgctag cctcctggct
 631 tcctcgattg gcgaaaaaac gtgttgtacc ccctagtaca ttgagcggaa ctagcaaccc ttggcctcga
 701 cttacttcgg tatggtttgc tgctcgcact gtggtgctac ggacatcgtt accgttgttg caacgcgttt
 771 gataattgac cgcttgatga atgagatcga agggccgttg ttaattatct gacctacctc cgcctatttc
 841 aacgtcctgg tgaagacgcg agccgggaag gccgaccgac caaataacga ctatttagac ctcggccact
 911 cgcacccaga gcgccatagt aacgtcgtga ccccggtcta ccattcggga gggcatagca tcaatagatg
 981 tgctgcccct cagtccgttg atacctactt gctttatctg tctagcgact ctatccacgg agtgactaat
1051 tcgtaaccat tgacagtctg gttcaaatga gtatatatga aatctaacta aattttgaag taaaaattaa
1121 attttcctag atccacttct aggaaaaact attagagtac tggttttagg gaattgcact caaaagcaag
1191 gtgactcgca gtctggggca tcttttctag tttcctagaa gaactctagg aaaaaaagac gcgcattaga
1261 cgacgaacgt ttgtttttct ggtggcgatg gtcgccacca aacaaacggc ctagttctcg atggttgaga
1331 aaaaggcttc cattgaccga agtcgtctcg cgtctatggt ttatgacagg aagatcacat cggcatcaat
1401 ccggtggtga agttcttgag acatcgtggc ggatgtatgg agcgagacga ttaggacaat ggtcaccgac
1471 gacggtcacc gctattcagc acagaatggc ccaacctgag ttctgctatc aatggcctat tccgcgtcgc
1541 cagcccgact tgccccccaa gcacgtgtgt cgggtcgaac ctcgcttgct ggatgtggct tgactctatg
1611 gatgtcgcac tcgatactct ttcgcggtgc gaagggcttc cctctttccg cctgtccata ggccattcgc
1681 cgtcccagcc ttgtcctctc gcgtgctccc tcgaaggtcc ccctttgcgg accatagaaa tatcaggaca
1751 gcccaaagcg gtggagactg aactcgcagc taaaaacact acgagcagtc cccccgcctc ggataccttt
1821 ttgcggtcgt tgcgccggaa aaatgccaag gaccggaaaa cgaccggaaa acgagtgtac aagaaaggac
1891 gcaatagggg actaagacac ctattggcat aatggcggaa actcactcga ctatggcgag cggcgtcggc
1961 ttgctggctc gcgtcgctca gtcactcgct ccttcgcctt ctcgcgggtt atgcgtttgg cggagagggg
2031 cgcgcaaccg gctaagtaat tacgtcgacc gtgctgtcca aagggctgac ctttcgcccg tcactcgcgt
2101 tgcgttaatt acactcaatc gagtgagtaa tccgtggggt ccgaaatgtg aaatacgaag gccgagcata
2171 caacacacct taacactcgc ctattgttaa agtgtgtcct ttgtcgatac tggtactaat gcggttcgac
2241 gtcgattatg ctgagtgata tccttgtccg gtggtaccct aggggcccat ggctcgagct taagtgaccg
2311 gcagcaaaat gttgcagcac tgacccttt gggaccgcaa tgggttgaat tagcggaacg tcgtgtaggg
2381 ggaaagcggt cgaccgcatt atcgcttctc cgggcgtggc tagcgggaag ggttgtcaac gcgtcggact
2451 taccgcttac cgcggactac gccataaaag aggaatgcgt agacacgcca taaagtgtgg cgtataccac
2521 gtgagagtca tgttagacga gactacggcg tatcaattcg gtcggggctg tgggcggttg tgggcgactg
2591 cgcgggactg cccgaacaga cgagggccgt aggcgaatgt ctgttcgaca ctggcagagg ccctcgacgt
2661 acacagtctc caaaagtggc agtagtggct ttgcgcgct
```

Figure 9

A6 scTCR-C-kappa cloned into pUC19-T7

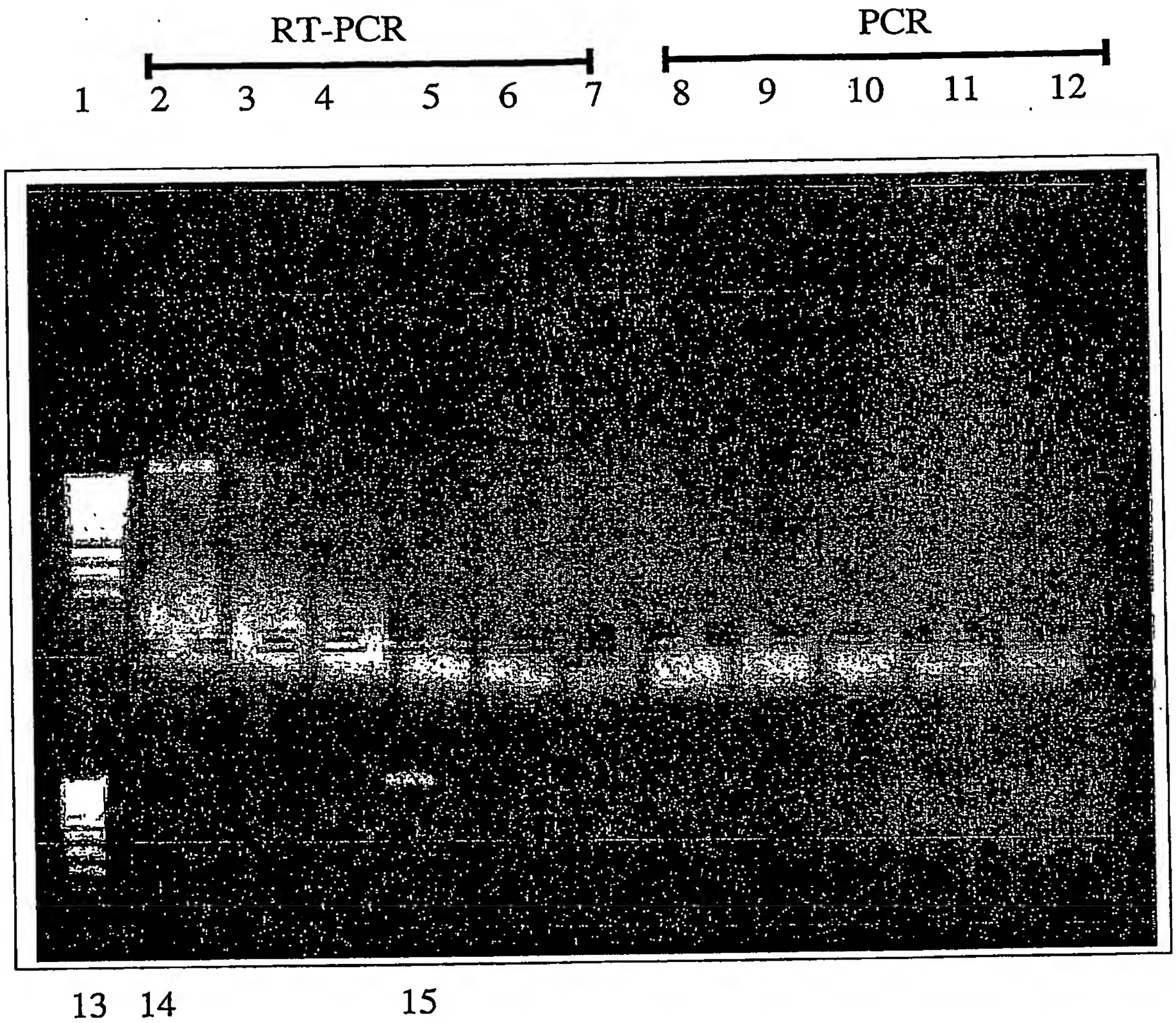
```
   1 ccatgggcca gaaggaagtg gagcagaact ctggacccct cagtgttcca
  51 gagggagcca ttgcctctct caactgcact tacagtgacc gaggttccca
 101 gtccttcttc tggtacagac aatattctgg gaaaagccct gagttgataa
 151 tgtccatata ctccaatggt gacaaagaag atggaaggtt tacagcacag
 201 ctcaataaag ccagccagta tgtttctctg ctcatcagag actcccagcc
 251 cagtgattca gccacctacc tctgtgccgt tacaactgac agctgggggа
 301 aattgcagtt tggagcaggg acccaggttg tggtcaccgg tggaggcggt
 351 tcaggcggag gtggatccgg cggtggcggg tcgaacgctg gtgtcactca
 401 gaccccaaaa ttccaggtcc tgaagacagg acagagcatg acactgcagt
 451 gtgcccagga tatgaaccat gaatacatgt cctggtatcg acaagaccca
 501 ggcatggggc tgaggctgat tcattactca gttggtgctg gtatcactga
 551 ccaaggagaa gtccccaatg gctacaatgt ctccagatca accacagagg
 601 atttcccgct caggctgctg tcggctgctc cctcccagac atctgtgtac
 651 ttctgtgcca gcaggccggg actagcggga gggcgaccag agcagtactt
 701 cgggccgggc accaggctca cggtcacaga ggacctgaaa aacgtgttcc
 751 cacccgaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc
 801 caaaaggcca cactggtgtg cctggccaca ggcttctacc ccgaccacgt
 851 ggagctgagc tggtgggtga atgggaagga ggtgcacagt ggggtcagca
 901 cagacccgca gcccctcaag gagcagcccg ccctcaatga ctccagatac
 951 gctctgagca gccgcctgag ggtctcggcc accttctggc aggaccccg
1001 caaccacttc cgctgtcaag tccagttcta cgggctctcg gagaatgacg
1051 agtggaccca ggatagggcc aaacccgtca cccagatcgt cagcgccgag
1101 gcctggggta gagcagacgg tggaggcggt tcactcagca gcaccctgac
1151 gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcgaagtca
1201 cccatcaggg cctgagttcg cccgtcacaa agagcttcaa ccgcggagag
1251 tcataagaat tc
```

Figure 10



The A6 scTCR-C-Kappa protein is shown in the above western blot with an arrow.

Figure 11



Lane 1 Bioline 100bp DNA marker
Lane 2 A6scTCR-C-Kappa reaction selected againt HLA-A2 TAX beads
Lane 3 A6scTCR-C-Kappa reaction selected againt HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR
Lane 4 A6scTCR-C-Kappa reaction selected againt control beads
Lane 5 Control no DNA reaction selected against HLA-A2-TAX beads
Lane 6 Control no DNA reaction selected againt HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR
Lane 7 Control no DNA reaction selected againt control beads
Lanes 8-12 and lane 13 are as lanes 2-7 except no rerverse transcriptase was added just Roche high fidelity taq. These are the DNA contamination controls.
Lane 13 RT-PCR positive control.

Figure 12a (Clone 9)

Clone 9 Mutated A6 TCR β chain DNA sequence

gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
gaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctccctcccagacatct
gtgtacttctgtgccagcaggccgggactagcgggagggtgaccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
cactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtgggg
tctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagac

Figure 12b (Clone 9)

Clone 9 Mutated A6 TCR β chain amino acid sequence

Agvtqtpkfqvlktgqsmtlqcaqdmnheymswyrqdpgmglrlihysvgagitdqgevpngynvsrsttedfplrllsaapsqts
vyfcasrpglagg*peqyfgpgtrltvtedlknvfppevavfepseaeishtqkatlvclatgfypdhvelswwvngkevhsgvctd
pqplkeqpalndsryalssrlrvsatfwqdprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgrad

* - Denotes the position of the amino acid corresponding to the introduced 'opal' stop codon, this will generally result in the substitution of a tryptophan (w) residue into the TCR β chain at this point.

Figure 13 (Clone 49)

Clone 49 Mutated A6 TCR β chain DNA sequence

gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgtagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
gaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctccctcccagacatct
gtgtacttctgtgccagcaggccgggactagcgggagggcgaccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
cactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtgggg
tctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagac

Figure 14a (Clone 134)

Clone 134 Mutated A6 TCR β chain DNA sequence
gctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaaccat
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgaccaagga
gaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctccctcccagacatct
gtgtacttctgtgcctcgaggccggggctg**atgagtgcggaa**ccagagcagtacttcgggccgggcaccaggctcacggtcac
agaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacccaaaaggcca
cactggtgtgcctggccaccggtttctaccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggggt
ctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgagcagccgcctgagggtctcgg
ccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccagga
tagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaagcttgaattc

Figure 14b (Clone 134)

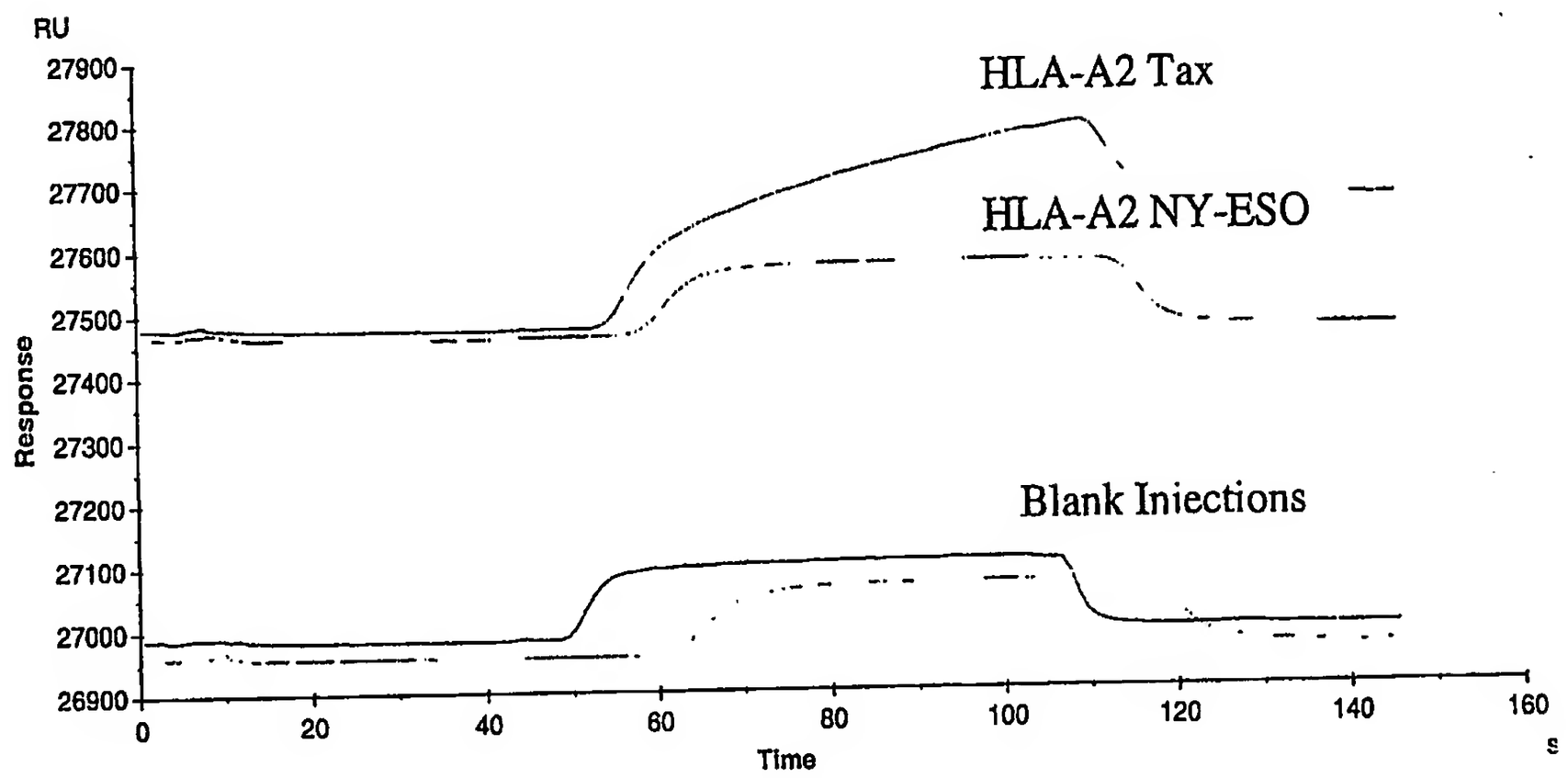
Clone 134A Mutated A6 TCR β chain amino acid sequence (BIAcore)
mnagvtqtpkfqvlktgqsmtlqcaqdmnheymswyrqdpgmglrlihysvgagitdqgevpngynvsrsttedfplrllsaaps
qtsvyfcasrpg**lmsae**peqyfgpgtrltvtedlknvfppevavfepseaeishtqkatlvclatgfypdhvelswwvngkevhsg
vctdpqplkeqpalndsryalssrlrvsatfwqdprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgrad*

Figure 14c (Clone 134)

Clone 134 Mutated A6 TCR β chain amino acid sequence (ELISA)
agvtqtpkfqvlktgqsmtlqcaqdmnheymswyrqdpgmglrlihysvgagitdqgevpngynvsrsttedfplrllsaapsqts
vyfcasrpg**lmsaq**peqyfgpgtrltvtedlknvfppevavfepseaeishtqkatlvclatgfypdhvelswwvngkevhsgvct
dpqplkeqpalndsryalssrlrvsatfwqdprnhfrcqvqfyglsendewtqdrakpvtqivsaeawgrad

Figure 15

A6 TCR clone 134



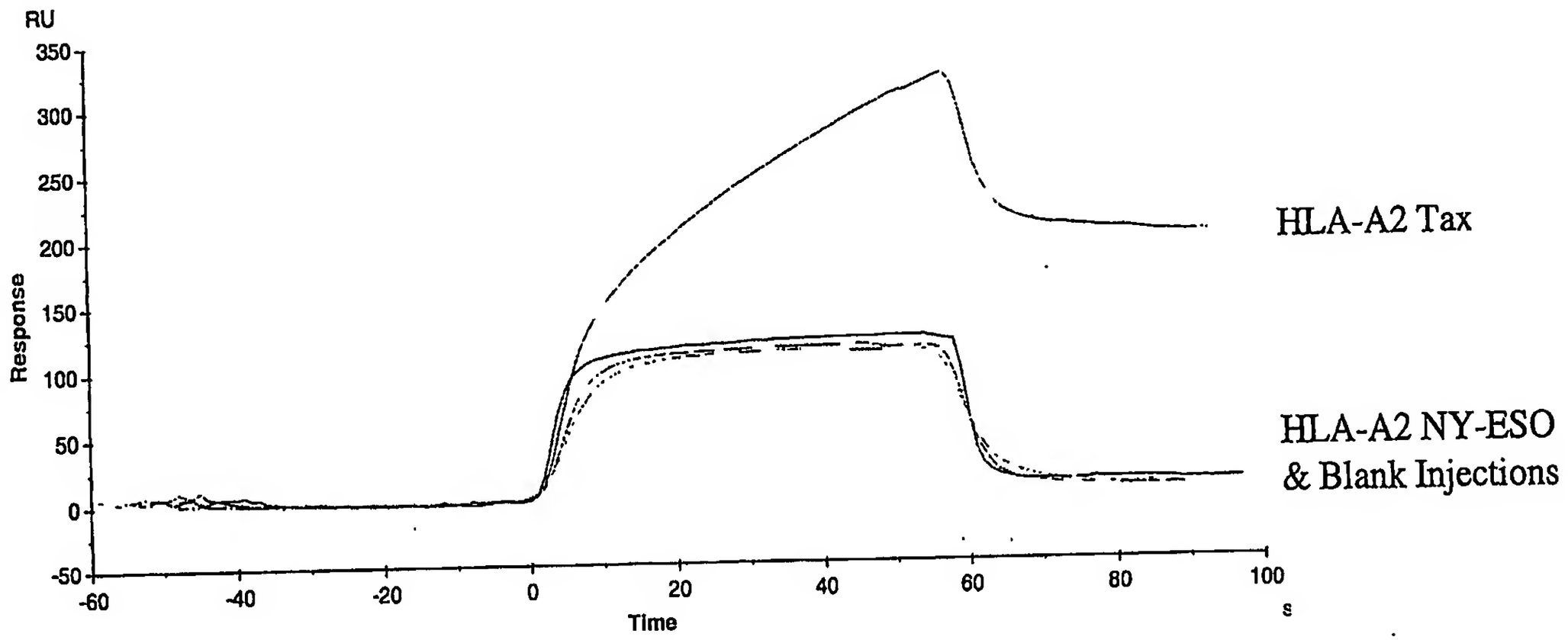
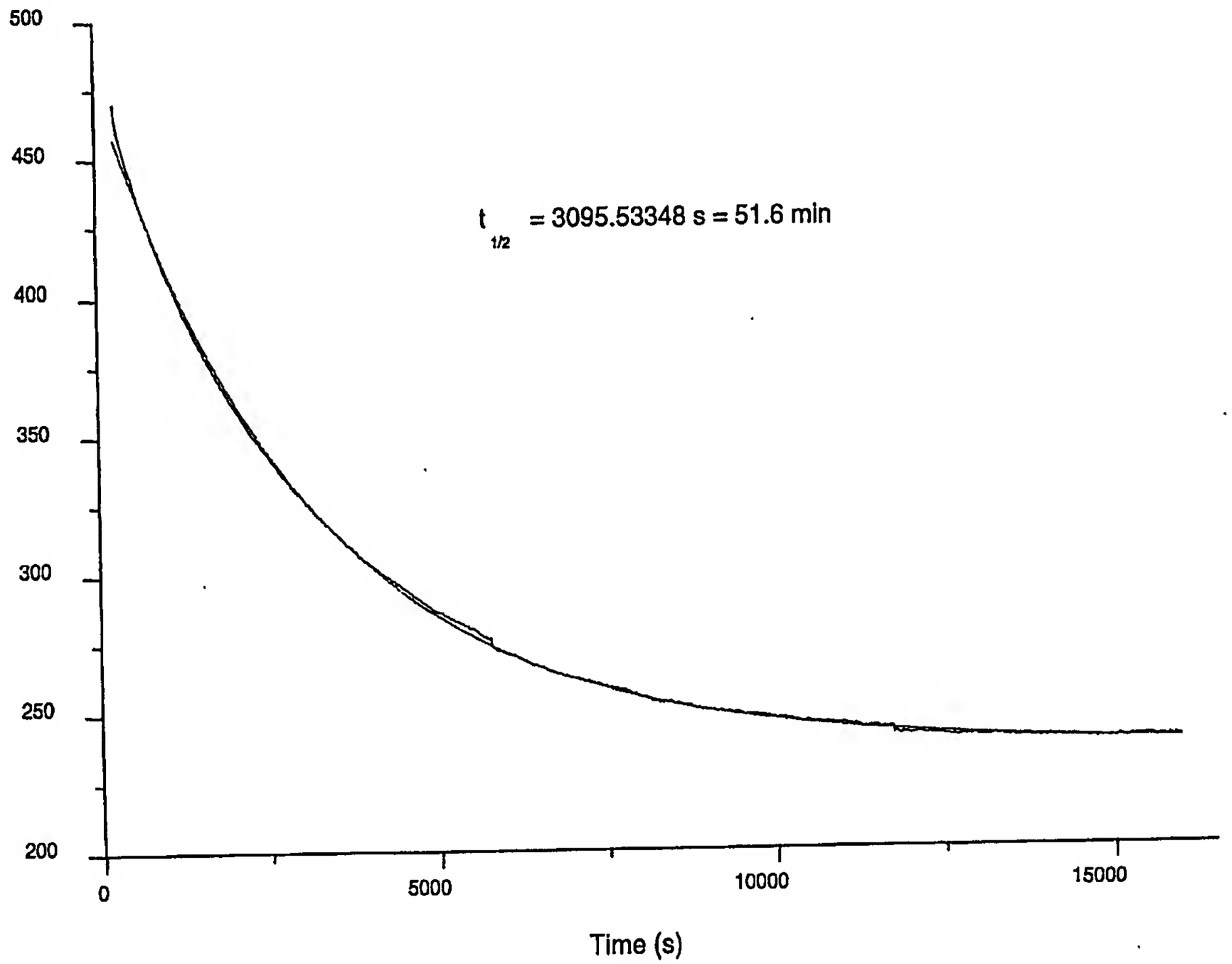


Figure 16



$t_{1/2}$ = 3095.53348 s = 51.6 min

Figure 17a

atgcaggaggygacacagattcctgcagctctgagtgtcccagaaggagaaaacttggttctcaactgcagtttcactgata
gcgctatttacaacctccagtggtttaggcaggaccctgggaaaggtctcacatctctgttgcttattcagtcaagtcagaga
gagcaaacaagtggaagacttaatgcctcgctggataaatcatcaggacgtagtactttatacattgcagcttctcagcctgg
tgactcagccacctacctctgtgctgtgaggcccacatcaggaggaagctacatacctacatttggaagaggaaccagcct
tattgttcatccgtatatccagaaccctgaccctgccgtgtaccagctgagagactctaaatccagtgacaagtctgtctgcct
attcaccgattttgattctcaaacaaatgtgtcacaaagtaaggattctgatgtgtatatcacagacaaatgtgtgctagacatg
aggtctatggacttcaagagcaacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaacaaca
gcattattccagaagacaccttcttccccagcccagaaagttcctaa

Figure 17b

atgggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagcatgacactgcagtgtgcccaggatatgaa
ccatgaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactg
accaaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccgctcaggctgctgtcggctgctc
cctcccagacatctgtgtacttctgtgccagcagttacgtcgggaacaccggggagctgttttttggagaaggctctaggctg
accgtactggaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatcagaagcagagatctcccacacc
caaaaggccacactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctggtgggtgaatgggaagg
aggtgcacagtggggtctgcacagacccgcagcccctcaaggagcagcccgccctcaatgactccagatacgctctgag
cagccgcctgagggtctcggccaccttctggcaggacccccgcaaccacttccgctgtcaagtccagttctacgggctctc
ggagaatgacgagtggacccaggatagggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcag
actaa

Figure 18a

MQEXTQIPAALSVPEGENLVLNCSFTDSAIYNLQWFRQ
DPGKGLTSLLLIQSSQREQTSGRLNASLDKSSGRSTLYI
AASQPGDSATYLCAVRPTSGGSYIPTFGRGTSLIVHPYI
QNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDS
DVYITDKCVLDMRSMDFKSNSAVAWSNKSDFACANAF
NNSIIPEDTFFPSPESS **Stop**

Figure 18b

MGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQ
DPG **Met** GLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDF
PLRLLSAAPSQTSVYFCASSYVGNTGELFFGEGSRLTVL
EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPD
HVELSWWVNGKEVHSGVCTDPQPLKEQPALNDSRYAL
SSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDR
AKPVTQIVSAEAWGRAD **Stop**

Figure 19

```
      1  TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTAATGTG AGTTAGCTCA
         AAGGACCGGA AAACGACCGG AAAACGAGTG TACATTACAC TCAATCGAGT
     51  CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG
         GAGTAATCCG TGGGGTCCGA ATGTGAAAT ACGAAGGCCG AGCATACAAC
    101  TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA
         ACACCTTAAC ACTCGCCTAT TGTTAAAGTG TGTCCTTTGT CGATACTGGT
    151  TGATTACGCC AAGCTACGTA CTTAAGTATT CTATTTCAAG GAGACAGTCA
         ACTAATGCGG TTCGATGCAT GAATTCATAA GATAAAGTTC CTCTGTCAGT
                K  Y    L  L  P    T  A  A  A    G  L  L    L  L  A
    201  TAATGAAATA CCTATTGCCT ACGGCAGCCG CTGGATTGTT ATTACTCGCG
         ATTACTTTAT GGATAACGGA TGCCGTCGGC GACCTAACAA TAATGAGCGC
                       NcoI                                PstI
                       ~~~~~~                              ~~~~~~~
          A  Q  P  A    M  A  K    Q  E  V    T  Q  I  P    A  A  L
    251  GCCCAGCCGG CCATGGCCAA ACAGGAGGTG ACGCAGATTC CTGCAGCTCT
         CGGGTCGGCC GGTACCGGTT TGTCCTCCAC TGCGTCTAAG GACGTCGAGA
                                                     PstI
                                                     ~~~~~~
          S  V  P    E  G  E  N    L  V  L    N  C  S    F  T  D  S
    301  GAGTGTCCCA GAAGGAGAAA ACTTGGTTCT CAACTGCAGT TTCACTGATA
         CTCACAGGGT CTTCCTCTTT TGAACCAAGA GTTGACGTCA AAGTGACTAT
          A  I  Y    N  L  Q    W  F  R  Q    D  P  G    K  G  L
    351  GCGCTATTTA CAACCTCCAG TGGTTTAGGC AGGACCCTGG GAAAGGTCTC
         CGCGATAAAT GTTGGAGGTC ACCAAATCCG TCCTGGGACC CTTTCCAGAG
          T  S  L  L    L  I  Q    S  S  Q    R  E  Q  T    S  G  R
    401  ACATCTCTGT TGCTTATTCA GTCAAGTCAG AGAGAGCAAA CAAGTGGAAG
         TGTAGAGACA ACGAATAAGT CAGTTCAGTC TCTCTCGTTT GTTCACCTTC
          L  N  A    S  L  D  K    S  S  G    R  S  T    L  Y  I  A
    451  ACTTAATGCC TCGCTGGATA AATCATCAGG ACGTAGTACT TTATACATTG
         TGAATTACGG AGCGACCTAT TTAGTAGTCC TGCATCATGA AATATGTAAC
          A  S  Q    P  G  D    S  A  T  Y    L  C  A    V  R  P
    501  CAGCTTCTCA GCCTGGTGAC TCAGCCACCT ACCTCTGTGC TGTGAGGCCC
         GTCGAAGAGT CGGACCACTG AGTCGGTGGA TGGAGACACG ACACTCCGGG
          T  S  G  G    S  Y  I    P  T  F    G  R  G  T    S  L  I
    551  ACATCAGGAG GAAGCTACAT ACCTACATTT GGAAGAGGAA CCAGCCTTAT
         TGTAGTCCTC CTTCGATGTA TGGATGTAAA CCTTCTCCTT GGTCGGAATA
                                BamHI
                                ~~~~~~~~
          V  H  P    Y  I  Q  N    P  D  P    A  V  Y    Q  L  R  D
    601  TGTTCATCCG TATATCCAGA ACCCGGATCC TGCCGTGTAC CAGCTGAGAG
         ACAAGTAGGC ATATAGGTCT TGGGCCTAGG ACGGCACATG GTCGACTCTC
          S  K  S    S  D  K    S  V  C  L    F  T  D    F  D  S
    651  ACTCTAAATC CAGTGACAAG TCTGTCTGCC TATTCACCGA TTTTGATTCT
         TGAGATTTAG GTCACTGTTC AGACAGACGG ATAAGTGGCT AAAACTAAGA
          Q  T  N  V    S  Q  S    K  D  S    D  V  Y  I    T  D  K
    701  CAAACAAATG TGTCACAAAG TAAGGATTCT GATGTGTATA TCACAGACAA
         GTTTGTTTAC ACAGTGTTTC ATTCCTAAGA CTACACATAT AGTGTCTGTT
          C  V  L    D  M  R  S    M  D  F    K  S  N    S  A  V  A
    751  ATGTGTGCTA GACATGAGGT CTATGGACTT CAAGAGCAAC AGTGCTGTGG
         TACACACGAT CTGTACTCCA GATACCTGAA GTTCTCGTTG TCACGACACC
          W  S  N    K  S  D    F  A  C  A    N  A  F    N  N  S
    801  CCTGGAGCAA CAAATCTGAC TTTGCATGTG CAAACGCCTT CAACAACAGC
         GGACCTCGTT GTTTAGACTG AAACGTACAC GTTTGCGGAA GTTGTTGTCG
                                                          AvrII
                                                          ~~
          I  I  P  E    D  T  F    F  P  S    P  E  S  S    *  *
    851  ATTATTCCAG AAGACACCTT CTTCCCCAGC CCAGAAAGTT CCTAATAACC
         TAATAAGGTC TTCTGTGGAA GAAGGGGTCG GGTCTTTCAA GGATTATTGG
         AvrII          EcoRI
         ~~~~           ~~~~~~
                                                  M    K  K  L
    901  TAGGTTAATT AAGAATTCTT TAAGAAGGGG ATATACATAT GAAAAAATTA
         ATCCAATTAA TTCTTAAGAA ATTCTTCCCC TATATGTATA CTTTTTTAAT
                                                  BssHII
                                                  ~~~~~~
          L  F  A  I    P  L  V    V  P  F    Y  S  H  S    A  Q  A
    951  TTATTCGCAA TTCCTTTAGT TGTTCCTTTC TATTCTCACA GCGCGCAGGC
         AATAAGCGTT AAGGAAATCA ACAAGGAAAG ATAAGAGTGT CGCGCGTCCG
          G  V  T    Q  T  P  K    F  Q  V    L  K  T    G  Q  S  M
   1001  TGGTGTCACT CAGACCCCAA AATTCCAGGT CCTGAAGACA GGACAGAGCA
         ACCACAGTGA GTCTGGGGTT TTAAGGTCCA GGACTTCTGT CCTGTCTCGT
               PstI
               ~~~~~~~~
          T  L  Q    C  A  Q    D  M  N  H    E  Y  M    S  W  Y
   1051  TGACACTGCA GTGTGCCCAG GATATGAACC ATGAATACAT GTCCTGGTAT
         ACTGTGACGT CACACGGGTC CTATACTTGG TACTTATGTA CAGGACCATA
          R  Q  D  P    G  M  G    L  R  L    I  H  Y  S    V  G  A
   1101  CGACAAGACC CAGGCATGGG GCTGAGGCTG ATTCATTACT CAGTTGGTGC
```

```
        GCTGTTCTGG GTCCGTACCC CGACTCCGAC TAAGTAATGA GTCAACCACG
        · G  I  T   D  Q  G  E   V  P  N   G  Y  N   V  S  R  S ·
1151    TGGTATCACT GACCAAGGAG AAGTCCCCAA TGGCTACAAT GTCTCCAGAT
        ACCATAGTGA CTGGTTCCTC TTCAGGGGTT ACCGATGTTA CAGAGGTCTA
        · T  T  E   D  F  P   L  R  L  L   S  A  A   P  S  Q
1201    CAACCACAGA GGATTTCCCG CTCAGGCTGC TGTCGGCTGC TCCCTCCCAG
        GTTGGTGTCT CCTAAAGGGC GAGTCCGACG ACAGCCGACG AGGGAGGGTC
         T  S  V  Y   F  C  A   S  S  Y   V  G  N  T   G  E  L ·
1251    ACATCTGTGT ACTTCTGTGC CAGCAGTTAC GTCGGGAACA CCGGGGAGCT
        TGTAGACACA TGAAGACACG GTCGTCAATG CAGCCCTTGT GGCCCCTCGA
        · F  F  G   E  G  S  R   L  T  V   L  E  D   L  K  N  V ·
1301    GTTTTTTGGA GAAGGCTCTA GGCTGACCGT ACTGGAGGAC CTGAAAAACG
        CAAAAAACCT CTTCCGAGAT CCGACTGGCA TGACCTCCTG GACTTTTTGC
                AvaI                                    BglII
                ~~~~~~~                                 ~~~~~~
        · F  P  P   E  V  A   V  F  E  P   S  E  A   E  I  S
1351    TGTTCCCACC CGAGGTCGCT GTGTTTGAGC CATCAGAAGC AGAGATCTCC
        ACAAGGGTGG GCTCCAGCGA CACAAACTCG GTAGTCTTCG TCTCTAGAGG
         H  T  Q  K   A  T  L   V  C  L   A  T  G  F   Y  P  D ·
1401    CACACCCAAA AGGCCACACT GGTGTGCCTG GCCACAGGCT TCTACCCCGA
        GTGTGGGTTT TCCGGTGTGA CCACACGGAC CGGTGTCCGA AGATGGGGCT
                                                  ApaLI
                                                  ~~~~~~~
        · H  V  E   L  S  W  W   V  N  G   K  E  V   H  S  G  V ·
1451    CCACGTGGAG CTGAGCTGGT GGGTGAATGG GAAGGAGGTG CACAGTGGGG
        GGTGCACCTC GACTCGACCA CCCACTTACC CTTCCTCCAC GTGTCACCCC
        · C  T  D   P  Q  P   L  K  E  Q   P  A  L   N  D  S
1501    TCTGCACAGA CCCGCAGCCC CTCAAGGAGC AGCCCGCCCT CAATGACTCC
        AGACGTGTCT GGGCGTCGGG GAGTTCCTCG TCGGGCGGGA GTTACTGAGG
         R  Y  A  L   S  S  R   L  R  V   S  A  T  F   W  Q  D ·
1551    AGATACGCTC TGAGCAGCCG CCTGAGGGTC TCGGCCACCT TCTGGCAGGA
        TCTATGCGAG ACTCGTCGGC GGACTCCCAG AGCCGGTGGA AGACCGTCCT
        · P  R  N   H  F  R  C   Q  V  Q   F  Y  G   L  S  E  N ·
1601    CCCCCGCAAC CACTTCCGCT GTCAAGTCCA GTTCTACGGG CTCTCGGAGA
        GGGGGCGTTG GTGAAGGCGA CAGTTCAGGT CAAGATGCCC GAGAGCCTCT
        · D  E  W   T  Q  D   R  A  K  P   V  T  Q   I  V  S
1651    ATGACGAGTG GACCCAGGAT AGGGCCAAAC CCGTCACCCA GATCGTCAGC
        TACTGCTCAC CTGGGTCCTA TCCCGGTTTG GGCAGTGGGT CTAGCAGTCG
                                                  XbaI
                                                  ~~~~~~
                                  NotI
                                  ~~~~~~~~~
         A  E  A  W   G  R  A   D  A  A   A
1701    GCCGAGGCCT GGGGTAGAGC AGACGCGGCC GCA
1702    CGGCTCCGGA CCCCATCTCG TCTGCGCCGG CGT
```

Figure 20

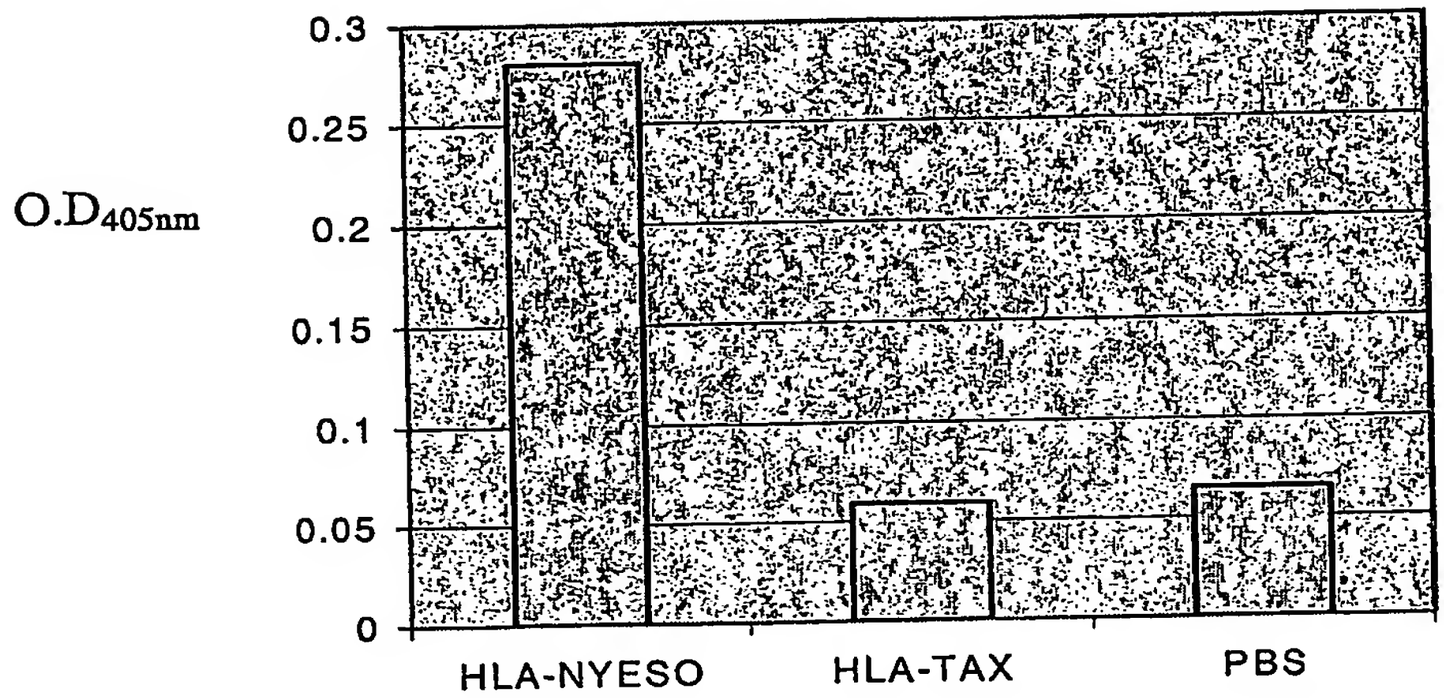


Figure 21

DRA0101

```
   1 ggatccatgg ccataagtgg agtccctgtg ctaggatttt tcatcatagc tgtgctgatg
  61 agcgctcagg aatcatgggc tatcaaagaa gaacatgtga tcatccaggc cgagttctat
 121 ctgaatcctg accaatcagg cgagtttatg tttgactttg atggtgatga gattttccat
 181 gtggatatgg caaagaagga gacggtctgg cggcttgaag aatttggacg atttgccagc
 241 tttgaggctc aaggtgcatt ggccaacata gctgtggaca aagccaacct ggaaatcatg
 301 acaaagcgct ccaactatac tccgatcacc aatgtacctc cagaggtaac tgtgctcacg
 361 aacagccctg tggaactgag agagcccaac gtcctcatct gtttcatcga caagttcacc
 421 ccaccagtgg tcaatgtcac gtggcttcga aatggaaaac ctgtcaccac aggagtgtca
 481 gagacagtct tcctgcccag ggaagaccac cttttccgca agttccacta tctccccttc
 541 ctgccctcaa ctgaggacgt ttacgactgc agggtggagc actggggctt ggatgagcct
 601 cttctcaagc actgggagtt tgatgctcca agccctctcc cagagactac agagaacgtg
 661 gatgggggtc tgactgatac acttccaagcg gagacagatc aacttgaaga caagaagtct
 721 gcgttgcaga ccgagattgc caatctactg aaagagaagg aaaaactaga gttcatcctg
 781 gcagcttacg gatctggtgg tggtctgaac gatatttttg aagctcagaa aatcgaatgg
 841 catgagtagg atcc
```

XXX - Fos Leucine zipper codons

XXX - Biotinylation tag codons

Figure 22

```
   1 aattctactc gtaaagcgag ttgaaggatc atatttagtt gcgtttatga gataagattg
  61 aaagcacgtg taaaatgttt cccgcgcgtt ggcacaacta tttacaatgc ggccaagtta
 121 taaaagattc taatctgata tgttttaaaa caccttgcg gcccgagttg tttgcgtacg
 181 tgactagcga agaagatgtg tggaccgcag aacagatagt aaaacaaaac cctagtattg
 241 gagcaataat cgatttaacc aacacgtcta aatattatga tggtgtgcat tttttgcggg
 301 cgggcctgtt atacaaaaaa attcaagtac ctggccagac tttgccgcct gaaagcatag
 361 ttcaagaatt tattgacacg gtaaaagaat ttacagaaaa gtgtcccggc atgttggtgg
 421 gcgtgcactg cacacacggt attaatcgca ccggttacat ggtgtgcaga tatttaatgc
 481 acaccctggg tattgcgccg caggaagcca tagatagatt cgaaaaagcc agaggtcaca
 541 aaattgaaag acaaaattac gttcaagatt tattaattta attaatatta tttgcattct
 601 ttaacaaata ctttatccta ttttcaaatt gttgcgcttc ttccagcgaa ccaaaactat
 661 gcttcgcttg ctccgtttag cttgtagccg atcagtggcg ttgttccaat cgacggtagg
 721 attaggccgg atattctcca ccacaatgtt ggcaacgttg atgttacgtt tatgcttttg
 781 gttttccacg tacgtctttt ggccggtaat agccgtaaac gtagtgccgt cgcgcgtcac
 841 gcacaacacc ggatgtttgc gcttgtccgc ggggtattga accgcgcgat ccgacaaatc
 901 caccactttg gcaactaaat cggtgacctg cgcgtctttt ttctgcatta tttcgtcttt
 961 cttttgcatg gtttcctgga agccggtgta catgcggttt agatcagtca tgacgcgcgt
1021 gacctgcaaa tctttggcct cgatctgctt gtccttgatg gcaacgatgc gttcaataaa
1081 ctcttgtttt ttaacaagtt cctcggtttt ttgcgccacc accgcttgca gcgcgtttgt
1141 gtgctcggtg aatgtcgcaa tcagcttagt caccaactgt ttgctctcct cctcccgttg
1201 tttgatcgcg ggatcgtact tgccggtgca gagcacttga ggaattactt cttctaaaag
1261 ccattcttgt aattctatgg cgtaaggcaa tttggacttc ataatcagct gaatcacgcc
1321 ggatttagta atgagcactg tatgcggctg caaatacagc gggtcgcccc ttttcacgac
1381 gctgttagag gtagggcccc cattttggat ggtctgctca aataacgatt tgtatttatt
1441 gtctacatga acacgtatag ctttatcaca aactgtatat tttaaactgt tagcgacgtc
1501 cttggccacg aaccggacct gttggtcgcg ctctagcacg taccgcaggt tgaacgtatc
1561 ttctccaaat ttaaattctc caattttaac gcgagccatt ttgatacacg tgtgtcgatt
1621 ttgcaacaac tattgttttt taacgcaaac taaacttatt gtggtaagca ataattaaat
1681 atgggggaac atgcgccgct acaacactcg tcgttatgaa cgcagacggc gccggtctcg
1741 gcgcaagcgg ctaaaacgtg ttgcgcgttc aacgcggcaa acatcgcaaa agccaatagt
1801 acagttttga tttgcatatt aacggcgatt ttttaaatta tcttatttaa taaatagtta
1861 tgacgcctac aactccccgc ccgcgttgac tcgctgcacc tcgagcagtt cgttgacgcc
1921 ttcctccgtg tggccgaaca cgtcgagcgg gtggtcgatg accagcggcg tgccgcacgc
1981 gacgcacaag tatctgtaca ccgaatgatc gtcgggcgaa ggcacgtcgg cctccaagtg
2041 gcaatattgg caaattcgaa aatatataca gttgggttgt ttgcgcatat ctatcgtggc
2101 gttgggcatg tacgtccgaa cgttgatttg catgcaagcc gaaattaaat cattgcgatt
2161 agtgcgatta aaacgttgta catcctcgct tttaatcatg ccgtcgatta aatcgcgcaa
2221 tcgagtcaag tgatcaaagt gtggaataat gttttctttg tattcccgag tcaagcgcag
2281 cgcgtatttt aacaaactag ccatcttgta agttagtttc atttaatgca actttatcca
2341 ataatatatt atgtatcgca cgtcaagaat taacaatgcg cccgttgtcg catctcaaca
2401 cgactatgat agagatcaaa taaagcgcga attaaatagc ttgcgacgca acgtgcacga
2461 tctgtgcacg cgttccggca cgagctttga ttgtaataag tttttacgaa gcgatgacat
2521 gacccccgta gtgacaacga tcacgcccaa aagaactgcc gactacaaaa ttaccgagta
2581 tgtcggtgac gttaaaacta ttaagccatc caatcgaccg ttagtcgaat caggaccgct
2641 ggtgcgagaa gccgcgaagt atggcgaatg catcgtataa cgtgtggagt ccgctcatta
2701 gagcgtcatg tttagacaag aaagctacat atttaattga tcccgatgat tttattgata
2761 aattgaccct aactccatac acggtattct acaatggcgg ggttttggtc aaaatttccg
2821 gactgcgatt gtacatgctg ttaacggctc cgcccactat taatgaaatt aaaaattcca
2881 attttaaaaa acgcagcaag agaaacattt gtatgaaaga atgcgtagaa ggaaagaaaa
2941 atgtcgtcga catgctgaac aacaagatta atatgcctcc gtgtataaaa aaaatattga
3001 acgatttgaa agaaaacaat gtaccgcgcg gcggtatgta caggaagagg tttatactaa
3061 actgttacat tgcaaacgtg gtttcgtgtg ccaagtgtga aaaccgatgt ttaatcaagg
3121 ctctgacgca tttctacaac cacgactcca agtgtgtggg tgaagtcatg catcttttaa
3181 tcaaatccca agatgtgtat aaaccaccaa actgccaaaa aatgaaaact gtcgacaagc
```

```
3241 tctgtccgtt tgctggcaac tgcaagggtc tcaatcctat ttgtaattat tgaataataa
3301 aacaattata aatgctaaat ttgtttttta ttaacgatac aaaccaaacg caacaagaac
3361 atttgtagta ttatctataa ttgaaaacgc gtagttataa tcgctgaggt aatatttaaa
3421 atcattttca aatgattcac agttaatttg cgacaatata attttatttt cacataaact
3481 agacgccttg tcgtcttctt cttcgtattc cttctctttt tcatttttct cctcataaaa
3541 attaacatag ttattatcgt atccatatat gtatctatcg tatagagtaa atttttgtt
3601 gtcataaata tatatgtctt ttttaatggg gtgtatagta ccgctgcgca tagtttttct
3661 gtaatttaca acagtgctat tttctggtag ttcttcggag tgtgttgctt taattattaa
3721 atttatataa tcaatgaatt tgggatcgtc ggttttgtac aatatgttgc cggcatagta
3781 cgcagcttct tctagttcaa ttacaccatt ttttagcagc accggattaa cataactttc
3841 caaaatgttg tacgaaccgt taaacaaaaa cagttcacct ccctttttcta tactattgtc
3901 tgcgagcagt tgtttgttgt taaaaataac agccattgta atgagacgca caaactaata
3961 tcacaaactg gaaatgtcta tcaatatata gttgctgatg atccagcatg ataagataca
4021 ttgatgagtt tggacaaacc acaactagaa tgcagtgaaa aaaatgcttt atttgtgaaa
4081 tttgtgatgc tattgcttta tttgtaacca ttataagctg caataaacaa gttccgagtt
4141 tgtcagaaag cagaccaaac agcggttgga ataatagcga gaacagagaa atagcggcaa
4201 aaataatacc cgtatcactt ttgctgatat ggttgatgtc atgtagccaa atcgggaaaa
4261 acgggaagta ggctcccatg ataaaaaagt aaaagaaaaa gaataaaccg aacatccaaa
4321 agtttgtgtt ttttaaatag tacataatgg atttccttac gcgaaatacg ggcagacatg
4381 gcctgcccgg ttattattat ttttgacacc agaccaactg gtaatggtag cgaccggcgc
4441 tcagctggaa ttcagatctg tgattgtaaa taaaatgtaa tttacagtat agtattttaa
4501 ttaatataca aatgatttga taataattct tatttaacta taatatattg tgttgggttg
4561 aattaaaggt cccggcatcc tcaaatgcat aatttcatag tccccccttgt tgtaagtgat
4621 gcgtatttct gaatctttgt aaaatagcac acaagactcc aacgcgtttg gcgttttatt
4681 ttcttgctcg actctagttt attaggcctc tagagatccg tatttatagg ttttttttatt
4741 acaaaactgt tacgaaaaca gtaaaatact tatttatttg cgagatggtt atcattttaa
4801 ttatctccat gatccaataa acctagaata aagggcccga cctttaattc aacccaacac
4861 aatatattat agttaaataa gaattattat caaatcattt gtatattaat taaaatacta
4921 tactgtaaat tacattttat ttacaatcac agatcccggg gatccggtta ttagtacatt
4981 tattaagcgc tagattctgt gcgttgttga tttacagaca attgttgtac gtattttaat
5041 aattcattaa atttataatc tttagggtgg tatgttagag cgaaaatcaa atgattttca
5101 gcgtctttat atctgaattt aaatattaaa tcctcaatag atttgtaaaa taggtttcga
5161 ttagtttcaa acaagggttg tttttccgaa ccgatggctg gactatctaa tggattttcg
5221 ctcaacgcca caaaacttgc caaatcttgt agcagcaatc tagctttgtc gatattcgtt
5281 tgtgttttgt tttgtaataa aggttcgacg tcgttcaaaa tattatgcgc ttttgtattt
5341 ctttcatcac tgtcgttagt gtacaattga ctcgacgtaa acacgttaaa taaagcttgg
5401 acatatttaa catcgggcgt gttagcttta ttaggccgat tatcgtcgtc gtcccaaccc
5461 tcgtcgttag aagttgcttc cgaagacgat tttgccatag ccacacgacg cctattaatt
5521 gtgtcggcta acacgtccgc gatcaaattt gtagttgagc tttttggaat tatttctgat
5581 tgcgggcgtt tttgggcggg tttcaatcta actgtgcccg attttaattc agacaacacg
5641 ttagaaagcg atggtgcagg cggtggtaac atttcagacg gcaaatctac taatggcggc
5701 ggtggtggag ctgatgataa atctaccatc ggtggaggcg caggcggggc tggcggcgga
5761 ggcggaggcg gaggtggtgg cggtgatgca gacggcggtt taggctcaaa tgtctcttta
5821 ggcaacacag tcggcacctc aactattgta ctggtttcgg gcgccgtttt tggtttgacc
5881 ggtctgagac gagtgcgatt tttttcgttt ctaatagctt ccaacaattg ttgtctgtcg
5941 tctaaaggtg cagcgggttg aggttccgtc ggcattggtg gagcgggcgg caattcagac
6001 atcgatggtg gtggtggtgg tggaggcgct ggaatgttag gcacgggaga aggtggtggc
6061 ggcggtgccg ccggtataat ttgttctggt ttagtttgtt cgcgcacgat tgtgggcacc
6121 ggcgcaggcg ccgctggctg cacaacggaa ggtcgtctgc ttcgaggcag cgcttggggt
6181 ggtggcaatt caatattata attggaatac aaatcgtaaa aatctgctat aagcattgta
6241 atttcgctat cgtttaccgt gccgatattt aacaaccgct caatgtaagc aattgtattg
6301 taaagagatt gtctcaagct cggatcgatc ccgcacgccg ataacaagcc ttttcatttt
6361 tactacagca ttgtagtggc gagacacttc gctgtcgtcg acgtacatgt atgctttgtt
6421 gtcaaaaacg tcgttggcaa gctttaaaat atttaaaaga acatctctgt tcagcaccac
6481 tgtgttgtcg taaatgttgt ttttgataat ttgcgcttcc gcagtatcga cacgttcaaa
```

6541 aaattgatgc gcatcaattt tgttgttcct attattgaat aaataagatt gtacagattc
6601 atatctacga ttcgtcatgg ccaccacaaa tgctacgctg caaacgctgg tacaatttta
6661 cgaaaactgc aaaaacgtca aaactcggta taaaataatc aacgggcgct ttggcaaaat
6721 atctatttta tcgcacaagc ccactagcaa attgtatttg cagaaaacaa tttcggcgca
6781 caattttaac gctgacgaaa taaaagttca ccagttaatg agcgaccacc caaattttat
6841 aaaaatctat tttaatcacg gttccatcaa caaccaagtg atcgtgatgg actacattga
6901 ctgtcccgat ttatttgaaa cactacaaat taaaggcgag ctttcgtacc aacttgttag
6961 caatattatt agacagctgt gtgaagcgct caacgatttg cacaagcaca atttcataca
7021 caacgacata aaactcgaaa atgtcttata tttcgaagca cttgatcgcg tgtatgtttg
7081 cgattacgga ttgtgcaaac acgaaaactc acttagcgtg cacgacggca cgttggagta
7141 ttttagtccg gaaaaaattc gacacacaac tatgcacgtt tcgtttgact ggtacgcggc
7201 gtgttaacat acaagttgct aaccggcggc cgacacccat ttgaaaaaag cgaagacgaa
7261 atgttggact tgaatagcat gaagcgtcgt cagcaataca atgacattgg cgttttaaaa
7321 cacgttcgta acgttaacgc tcgtgacttt gtgtactgcc taacaagata caacatagat
7381 tgtagactca caaattacaa acaaattata aaacatgagt ttttgtcgta aaaatgccac
7441 ttgttttacg agtagaattc ccagcttggc actggccgtc gttttacaac gtcgtgactg
7501 ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catccccctt tcgccagctg
7561 gcgtaatagc gaagaggccc gcaccgatcg ccccttcccaa cagttgcgca gcctgaatgg
7621 cgaatggcgc ctgatgcggt attttctcct tacgcatctg tgcggtattt cacaccgcat
7681 atggtgcact ctcagtacaa tctgctctga tgccgcatag ttaagccagc cccgacaccc
7741 gccaacaccc gctgacgcgc cctgacgggc ttgtctgctc ccggcatccg cttacagaca
7801 agctgtgacc gtctccggga gctgcatgtg tcagaggttt tcaccgtcat caccgaaacg
7861 cgcggacgaa agggcctcgt gatacgccta tttttatagg ttaatgtcat gataataatg
7921 gtttcttaga cgtcaggtgg cacttttcgg ggaaatgtgc gcggaacccc tatttgttta
7981 tttttctaaa tacattcaaa tatgtatccg ctcatgagac aataaccctg ataaatgctt
8041 caataatatt gaaaaaggaa gagtatgagt attcaacatt tccgtgtcgc ccttattccc
8101 ttttttgcgg cattttgcct tcctgttttt gctcacccag aaacgctggt gaaagtaaaa
8161 gatgctgaag atcagttggg tgcacgagtg ggttacatcg aactggatct caacagcggt
8221 aagatccttg agagttttcg ccccgaagaa cgttttccaa tgatgagcac ttttaaagtt
8281 ctgctatgtg gcgcggtatt atcccgtatt gacgccgggc aagagcaact cggtcgccgc
8341 atacactatt ctcagaatga cttggttgag tactcaccag tcacagaaaa gcatcttacg
8401 gatggcatga cagtaagaga attatgcagt gctgccataa ccatgagtga taacactgcg
8461 gccaacttac ttctgacaac gatcggagga ccgaaggagc taaccgcttt tttgcacaac
8521 atgggggatc atgtaactcg ccttgatcgt tgggaaccgg agctgaatga agccatacca
8581 aacgacgagc gtgacaccac gatgcctgta gcaatggcaa caacgttgcg caaactatta
8641 actggcgaac tacttactct agcttcccgg caacaattaa tagactggat ggaggcggat
8701 aaagttgcag gaccacttct gcgctcggcc cttccggctg gctggtttat tgctgataaa
8761 tctggagccg gtgagcgtgg gtctcgcggt atcattgcag cactggggcc agatggtaag
8821 ccctcccgta tcgtagttat ctacacgacg gggagtcagg caactatgga tgaacgaaat
8881 agacagatcg ctgagatagg tgcctcactg attaagcatt ggtaactgtc agaccaagtt
8941 tactcatata tactttagat tgatttaaaa cttcattttt aatttaaaag gatctaggtg
9001 aagatccttt ttgataatct catgaccaaa atcccttaac gtgagttttc gttccactga
9061 gcgtcagacc ccgtagaaaa gatcaaagga tcttcttgag atccttttt tctgcgcgta
9121 atctgctgct tgcaaacaaa aaaaccaccg ctaccagcgg tggtttgttt gccggatcaa
9181 gagctaccaa ctcttttttcc gaaggtaact ggcttcagca gagcgcagat accaaatact
9241 gtccttctag tgtagccgta gttaggccac cacttcaaga actctgtagc accgcctaca
9301 tacctcgctc tgctaatcct gttaccagtg gctgctgcca gtggcgataa gtcgtgtctt
9361 accgggttgg actcaagacg atagttaccg gataaggcgc agcggtcggg ctgaacgggg
9421 ggttcgtgca cacagcccag cttggagcga acgacctaca ccgaactgag atacctacag
9481 cgtgagcatt gagaaagcgc cacgcttccc gaagggagaa aggcggacag gtatccggta
9541 agcggcaggg tcggaacagg agagcgcacg agggagcttc cagggggaaa cgcctggtat
9601 ctttatagtc ctgtcgggtt tcgccacctc tgacttgagc gtcgattttt gtgatgctcg
9661 tcagggggggc ggagcctatg gaaaaacgcc agcaacgcgg cctttttacg gttcctggcc
9721 ttttgctggc cttttgctca catgttcttt cctgcgttat cccctgattc tgtggataac
9781 cgtattaccg cctttgagtg agctgatacc gctcgccgca gccgaacgac cgagcgcagc
9841 gagtcagtga gcgaggaagc ggaagagcgc ccaatacgca aaccgcctct ccccgcgcgt
9901 tggccgattc attaatgcag ctggcacgac aggtttcccg actggaaagc gggcagtgag
9961 cgcaacgcaa ttaatgtgag ttagctcact cattaggcac cccaggcttt acactttatg

```
10021 cttccggctc gtatgttgtg tggaattgtg agcggataac aatttcacac aggaaacagc
10081 tatgaccatg attacg
```

XXX - Restriction enzyme sites

Figure 23

```
   1 ggtaccggat ccagcatggt gtgtctgaag ctccctggag gctcctgcat gacagcgctg
  61 acagtgacac tgatggtgct gagctcccca ctggctttgt ccggagacac cggacctaag
 121 tacgtcaagc agaacacact gaaactggct tccggtggcg gatctctagt tccacgcggt
 181 agtggaggcg gtggttccgg agacacgcgt ccacgtttct tgtggcagct taagtttgaa
 241 tgtcatttct tcaatgggac ggagcgggtg cggttgctgg aaagatgcat ctataaccaa
 301 gaggagtccg tgcgcttcga cagcgacgtg ggggagtacc gggcggtgac ggagctgggg
 361 cggcctgatg ccgagtactg gaacagccag aaggacctcc tggagcagag gcgggccgcg
 421 gtggacacct actgcagaca caactacggg gttggtgaga gcttcacagt gcagcggcga
 481 gttgagccta aggtgactgt gtatccttca aagacccagc ccctgcagca ccacaacctc
 541 ctggtctgct ctgtgagtgg tttctatcca ggcagcattg aagtcaggtg gttccggaac
 601 ggccaggaag agaaggctgg ggtggtgtcc acaggcctga tccagaatgg agattggacc
 661 ttccagaccc tggtgatgct ggaaacagtt cctcggagtg gagaggttta cacctgccaa
 721 gtggagcacc caagtgtgac gagccctctc acagtggaat ggagagcacg gtctgaatct
 781 gcacagagca aggtcgacgg aggcggtggg ggtagaatcg cccggctgga ggaaaaagtg
 841 aaaaaccttga aagctcagaa ctcggagctg gcgtccacgg ccaacatgct tcagggaacag
 901 gtggcacagc ttaaacagaa agtcatgaac tactaggatc c
```

xxx - Jun Leucine zipper codons

xxx - HLA-loaded peptide

Figure 24

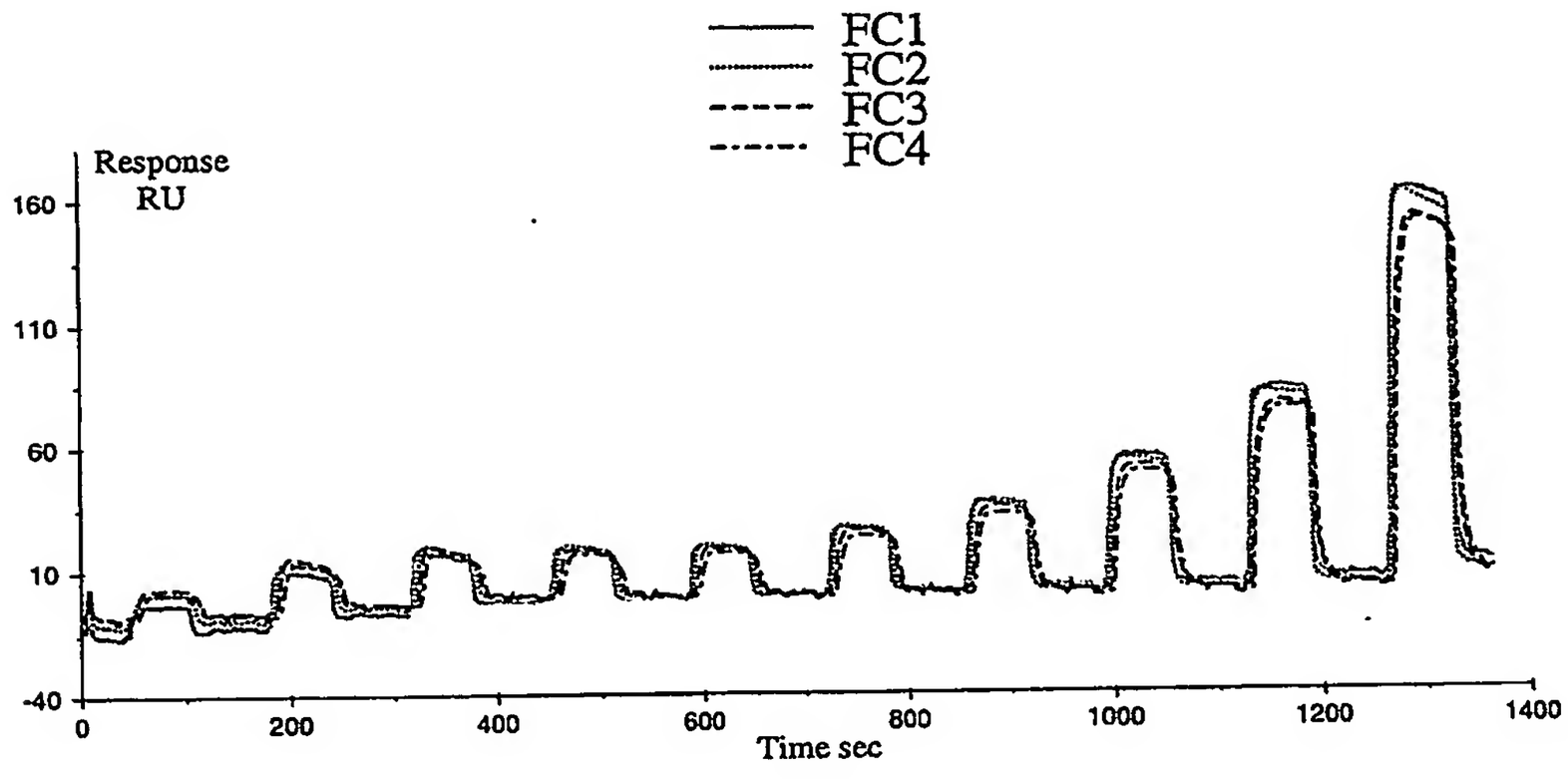

FC1
FC2
FC3
FC4
Response
RU
160
110
60
10
-40
0
200
400
600
800
1000
1200
1400
Time sec

Figure 25

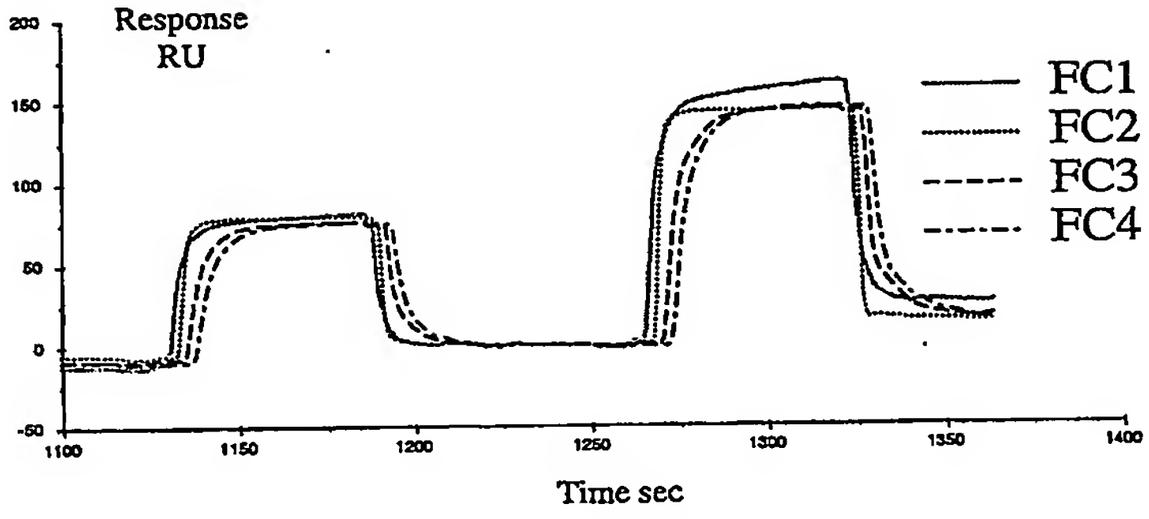

Response
RU
200
150
100
50
0
-50
1100
1150
1200
1250
1300
1350
1400
FC1
FC2
FC3
FC4
Time sec

Figure 26

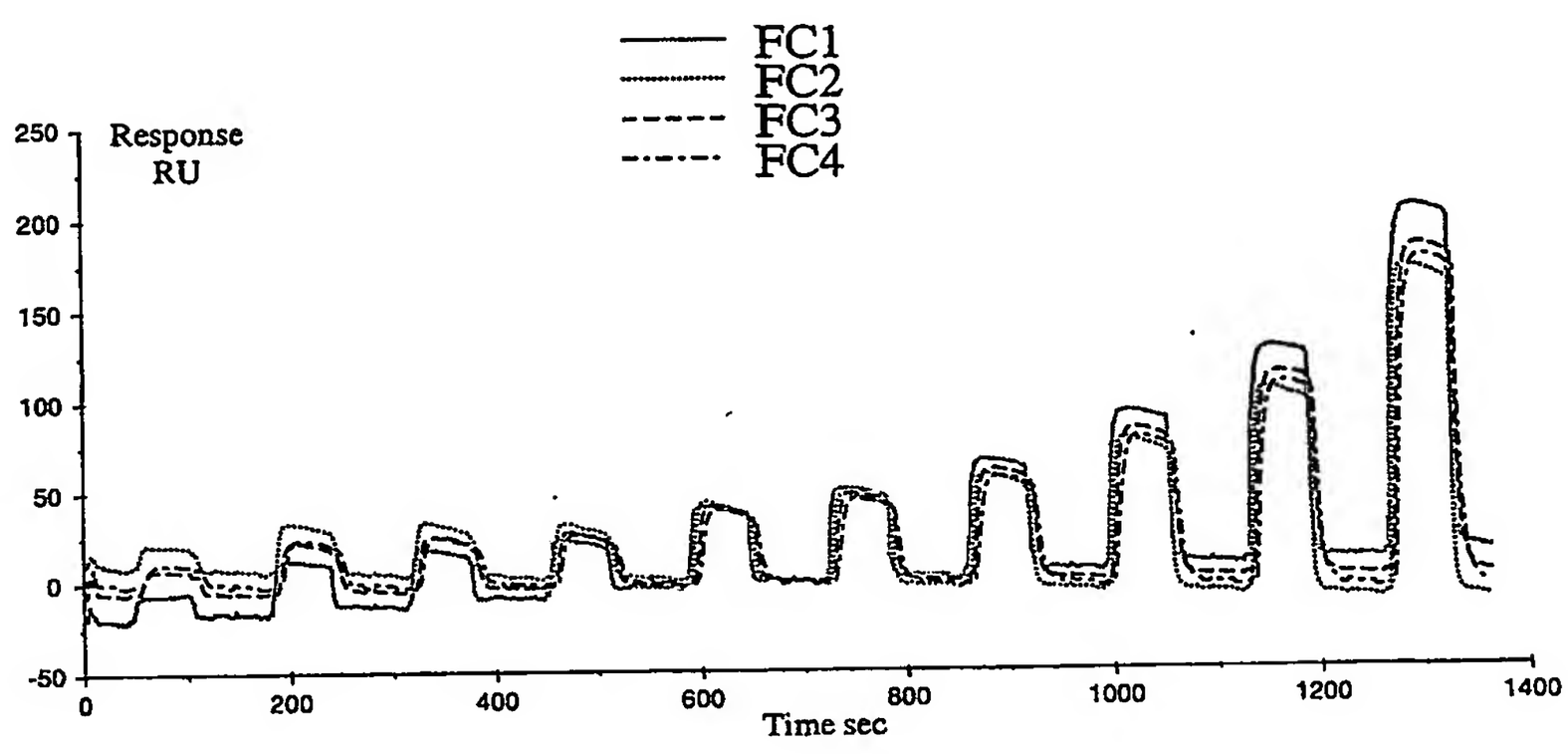

FC1
FC2
FC3
FC4
Response
RU
250
200
150
100
50
0
-50
0
200
400
600
800
1000
1200
1400
Time sec

Figure 27

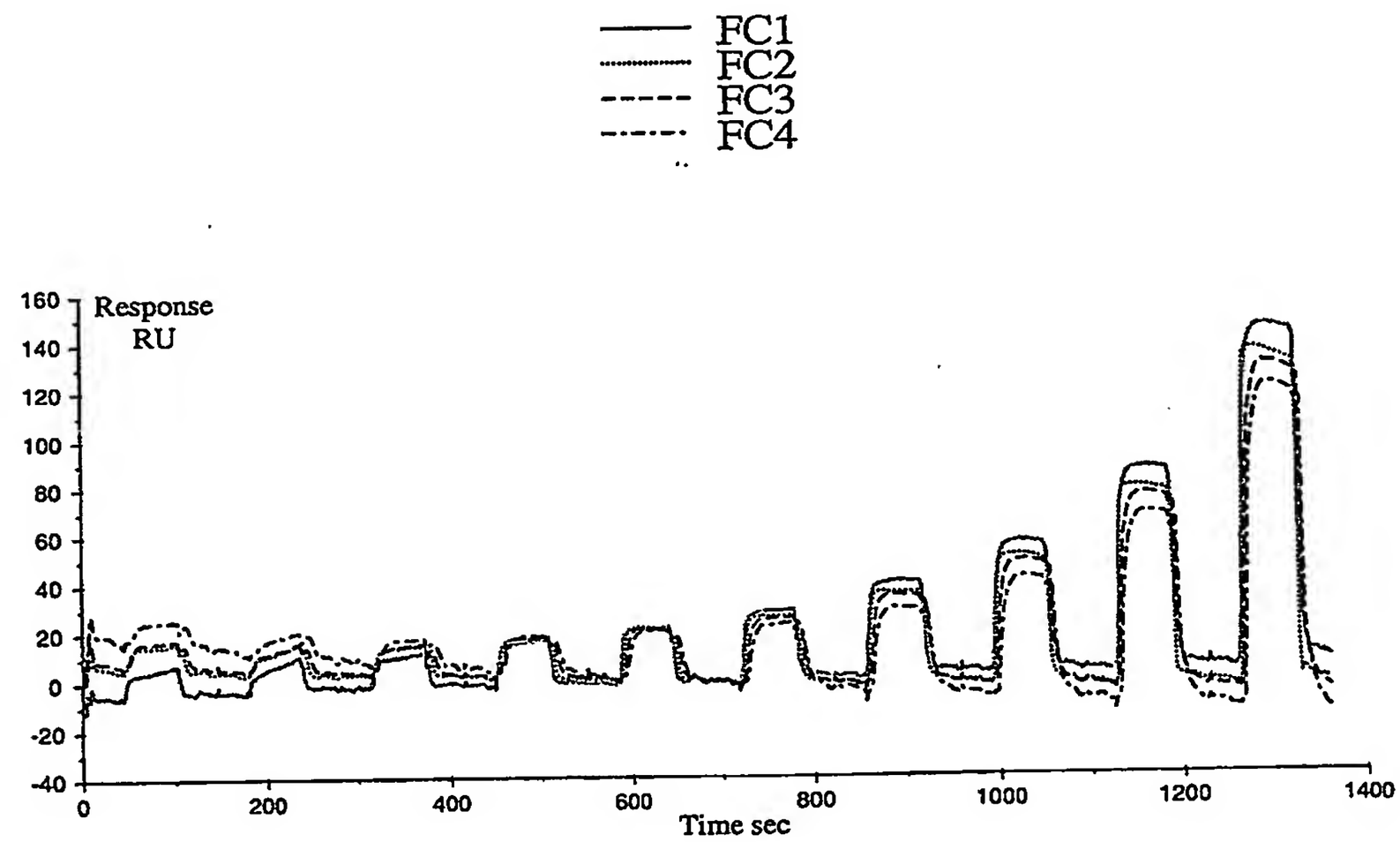
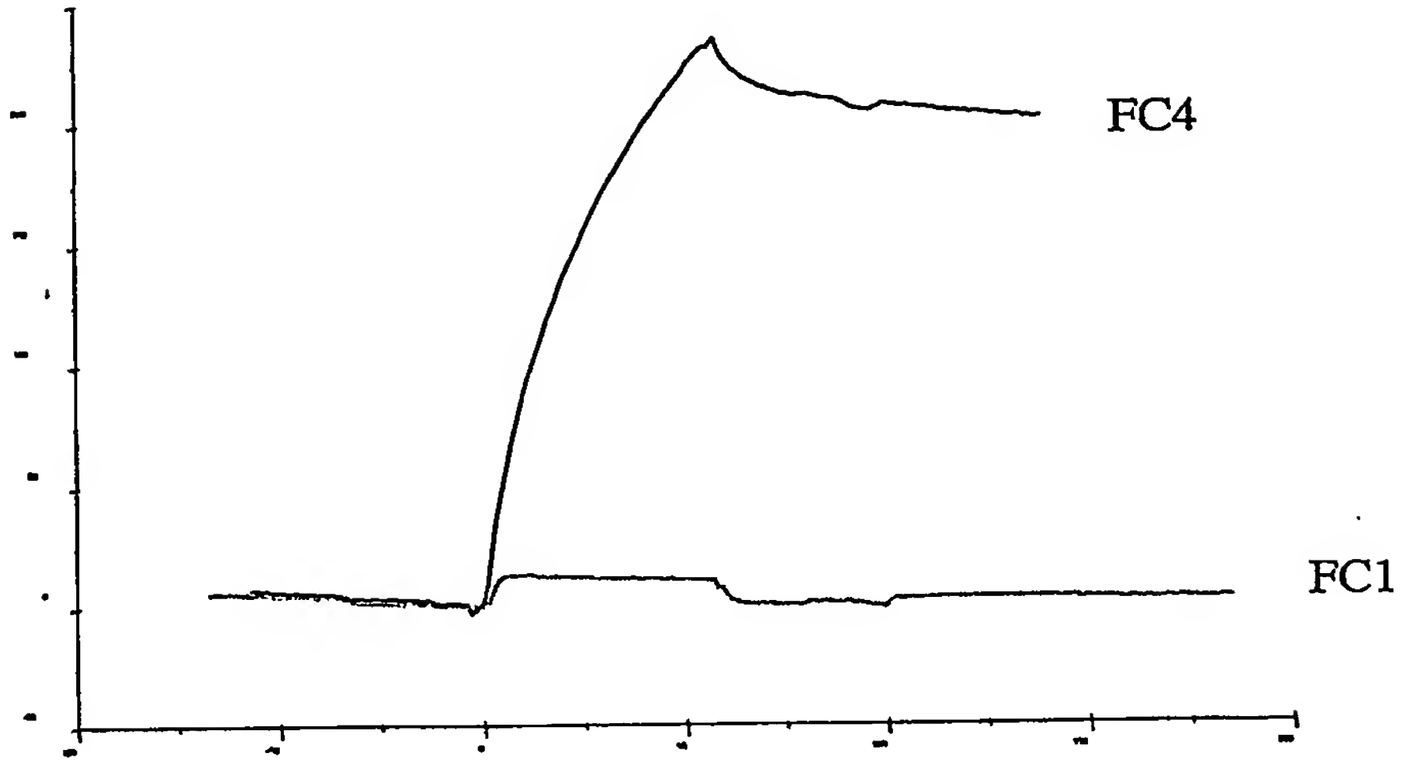

FC1
FC2
FC3
FC4
Response
RU
160
140
120
100
80
60
40
20
0
-20
-40
0
200
400
600
800
1000
1200
1400
Time sec

Figure 28



PCT Application
GB0304636